U.S. DEPARTMENT OF COMMERCE.
Patent and Trademark Office

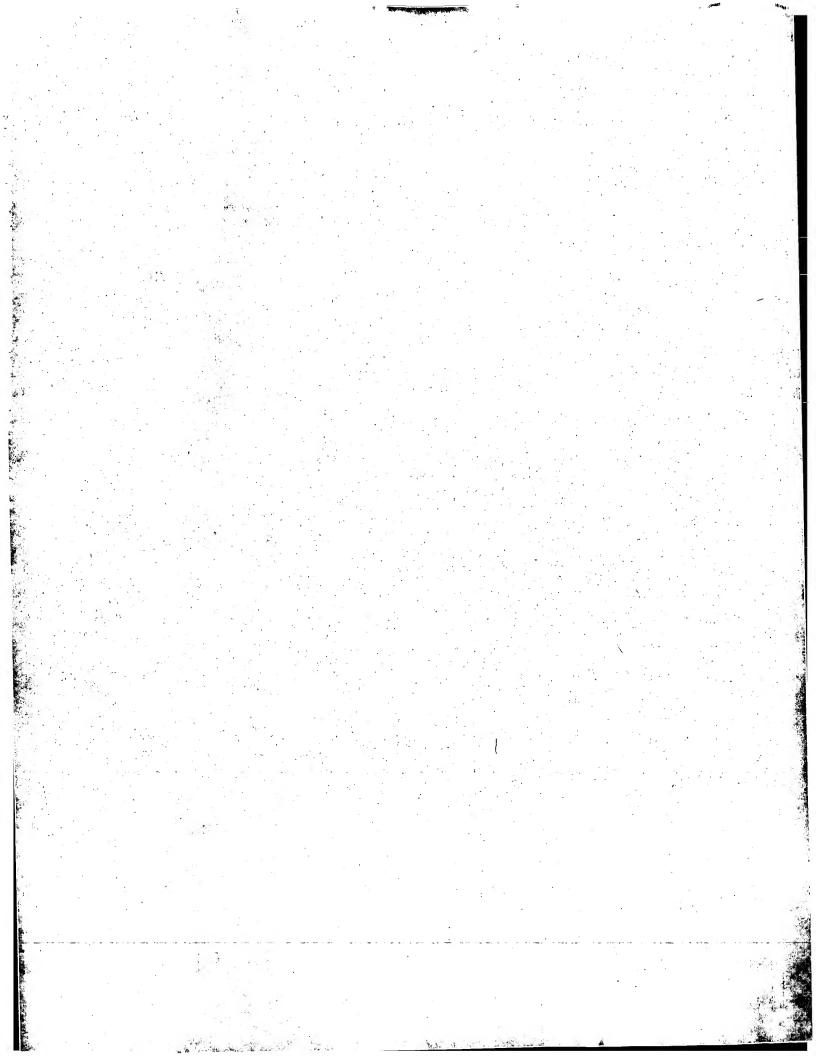
## SEARCH REQUEST FORM

Requestor's Name:	- 37 -		Serial _ Number: _		
Date:		Phone:		Art Unit:	
Search Topic: Please write a detailed s that may have a special a copy of the sequence.	meaning. Give example	es or relevant citation	is, authors keywords	, etc., if known. For se	hed. Define any terms quences, please attach
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Other

Bibliographic



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OM nucleic - nucleic search, using sw model

January 16, 2003, 09:50:52; Search time 6615.05 Seconds Run on:

17527.554 Million cell.updates/sec

US-09-763-334-1 3984 1,acctttgggttgctgggacg.....agagtttttgaaatttttt 3984 Title: Perfect score: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

2054640 seqs, 14551402878 residues Searched:

4109280 Total number of hits satisfying chosen parameters:

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em\_htgo\_mus:\*
em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	455	Ношо	041	56 Seque	AFIU4414 Mus muscu	ATESSOCS HIMS PROTE		_	Mus mu	6 wa	Sedneuce	AB023958 Mus	Human	man t	AFZU/24/ HOMO Sapi	Mus	AC126128 Rattus no		3 Rattus	3 Rattus	L39837 Drosophila	029608 Drosophila	AL356285 Human DNA	Euplot			Seque	SCUZBBUS HOMO SAPI		cryst	AY128279 Arabidops			34 Caenorh	Š.	R084691	H.sapie	385	096444	063969 Arabido	_	
SUMMARIES	QI	AR2014	AF10441	AF16404	AR20145	AFIU	E24013	F24614	7 AF119846	AC102712	E24616	AR201457		E38226		AF 20/34	AC10271	AC1261		AC09862	AC09862	DROWART	DMU2960	AL356285		E0C24968				AB023182		AY12827	EOC249	E0C2496	AF275	A52140	Κ.	HSPROKI	BC01208	AY09644	AYUb3	ECU4767	
, QN	Match Length DB	0.0 3984	6.6	.8 4241	2.3 3213	2.3 3213	0.8 2442	1374	23.4 1807 17	1.3 164490	9.8 795	9.1 3155	9.1 3460	.7 5486	./ 5486	.6 4098	1 164490	.2 191604	.6 582	.2 181750	.6 181750	.8 5360	07/5 8.	8.5 183597 9	.1 1322	.1 1578	.9 1804	.8 1935	4/25	8 5181	2202	.4 2422	.4 1606	.4 1314	.4 1745	.4 3018	018	3018	3593	738	2365	1807	
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ALIGNMENTS

DNA AR201455 Sequence 3 from patent US 6359193 AR201455 AR201455.1 GI:20252343 Jnknown RESULT 1
AR201455
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

PAT 20-APR-2002

linear

Nucleotide sequences of Patent: US 6359193-A 3 Inclassified REFERENCE AUTHORS TITLE JOURNAL FEATURES

Jnknown

ORGANISM

nknown" 798 g 1059 Score 3984; Pred. No. 0
ACCTTTGGGTTGCTGGGACGGACTCTGGCCGCCTCAGCGTCCGCCTCAGGCCCGTGGCC 
SCTGTCCAGGAGCTCTGCTCCCCCCCCCAGAGTTAATTATTTAT
ACAGICCIGGGGACIICCIIGAAGGAICAIIIIIIIIII
TCTA CAAATAAAGAAGTCCTTCGTGTGGGCTACATATATAGATGTTTTCATGAAGAGGA 
GTGAAAAGCCAGAAGGATATAGACAAATGAGGCCTAAGACCTTTCCTGCCAGTAACTATA 
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CCTTAGTTCCTCAGAGGCATGGCCGCACTAGGAGAAAGTGTGGCCTATCATTCTGAGA 
GTCCCAACTCACAGACAGATGTAGGAAGACCTTTGTCTGGATCTGGTATATCAGCATTTG 
TTCAAGCTCACCCTAGCAACGGACAGAGAGAGAACCCCCCCC

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2041	10	2161	2221	2281	2341	2401	2461 2461	2521 2521	2581 2581	2641	2701	2761 2761	2821 2821	2881 2881	2941	3001	3061	3121
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	Db 312	1 ACTGGCAAACATCTTCACATTCCACCACAAGCTAAACTCAGTCCTGAAGCTTCTGATC 31	180
	Qy 318	1 TTATTATAAACTTTGCCGAGGACCCGAAGATCGCTTAGGCAAGAATGGTGGTGGAA 32	240
	.Db 318	TTATTATTATAAACTTTGCCGAGGACCCGAAGATCGCTTAGGCAAGAATGCTGCTGATGAAA 3	1240
	324	1 TAAAAÖCTCATCCATTTTTAAAACAATTGACTTCTCCAGTGACCTGAGAGAGTGG 3	30
	Db 324	1 TAAAAGCTCATCCATTTTTTAAAACAATTGACTTCTCCAGTGACCTGAGACAGCAGTCTG 3	1300
,	m .	.CTTCATACATTCCTAAAATCACACCCAACAGATACATCATTGATCTGTGATC 3	36
•	י י	CIICAIACAIICCIAAAAICACACCCAACAGAIACAICAAAIIIIGAICCIGIIGAIC	9
	Oy 3361	CTGATAAATTATGGAGTGATGATAACGAGGAAGAAATGTAAATGACACTCTCAATGGAT 3 	420
	342	GGTATATAAAAATGGAAAGCATCCTGAACATGCATTCTATGAATTTTTTTT	. 4
	342		48
	_ Qy 348]	. (1)	
	Db 3481	1 TTGATGACAATGGCTACCCATATAATTATCCGAAGCCTATTGAATATGAATACATTAATT 35	1540
	Qy. 354]	1 CACAAGGCTCAGAGCAGCGGTCGGATGAAGATGATCAAAACACAGGCTCAGAGATTAAAA 36	0091
	Db 3541	3	009
	оу 3601 Db 3601	ATCGCGATCTAGTATATGTTTAACACACTAGTAAATAAAT	1660
	Qy 3661	GGCCTGAAATGCGAGGTGTTTTGAGGTTCTGAGAGTAAAATTATGCAAAATATGACAGAGC 3	72
	Db 3661		720
	Oy 3721	1 TATATATGTGCTGCTCTGTGTACAATATTTTATTTTCTAAATTATGGGAAATCCTTTTAA 37	1780
	. pb 3721	3	1780
	378	AATGTTAATTTATTCCAGCCGTTTAAATCAGTATTTAGAAAAAATTGTTATAAGGAAAG 3	84
	378	AATGTTAATTTATTCCAGCCGTTTAAATCAGTATTTAGAAAAAATTGTTATAAGGAAAG 3	84
	Qy 3841	1 TAAATTATGAACTGAATATTATAGTCAGTTCTTGGTACTTAAAGTACTTAAAATAGT 39	0061
	Db 3841	m	,0061
	æ	1 TGCTTTGTTTAAAAGGAGAAACCTGGTATCTATTTGTATATATGTAATAATTTTAAAA 3	96
	Db 3901	TGCTTTGTTTAAAAGGAGAAACCTGGTATCTATTTGTATATATGCTAAATAATTTTAAAA 3	096
	396	TACAAGAGTTTTTGAAATTTTTT 398	
	. 396.	ACAAGAGTTTTTGAAATTTTTTT 3984	
	RESULT 2 AF104413 LOCUS	13 4307 bp mRNA linear PRI 18-	3-1
	DEFINITION ACCESSION	Homo sapiens large tumor suppressor AF104413	cds.
	KEYWORDS		
	ORGANIS	nomo saptens Homo saptens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos	tomi;
	REFERENCE	Mammalia: Eutheria: Primates; Catarrhini; Hominidae; 1 (bases 1 to 4307) (bases 1 to 4307).	
	TITLE		hila

381 TGTCCAGGAGCTCTGCTCCCCCCCCCAGAGTTAATTATTATATTGTAAAGAATTTTAAC 440

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SSKFNFPSGRPGMQNGTGQTDFMIHQNVVPAGTVNRQPPPPYPLTAANGQSPSALQTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GISAFVQAHPSNGQRVNPPPPPQVRSVTPPPPPRGQTPPPRGTTPPPPSWEPNSQTKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSAAPSSYTNGSIPQSMMVPNRNSHNMELYNISVPGLQTNWPQSSSAPAQSSPSSGHE
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THPTDTSNFDPVDPDKLWSDDNEEENVNDTLNGWYKNGKHPEHAFYEFTFRRFFDDNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MKRSEKPEGYRQMRPKTFPASNYTVSSRQMLQEIRESLRNLSKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDAAKAEHNMSKMSTEDPRQVRNPPKFGTHHKALQEIRNSLLPFANETNSSRSTSEVN
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                                                                                                                                                                          St John, M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                  3. (bases 1 to 4307)
St John,M.A., Tao,W., Fel,X., Fukumoto,R., Carcangiu,M.L.,
St John,M.A., G., Parlow,A.F., McGrath,J. and Xu,T.
Mice deficient of Lats1 develop soft-tissue sarcomas, ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tao,W. and Xu,T.
Direct Submission
Submitted (04-NNV-1998) Genetics, HHMI, Yale University, 295
Submitted (04-NNV-1948) Maw Haven, CT 06536, USA
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                                                                                                                                                                          Stewart, R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="large tumor suppressor 1"
/protein_id="AAD16882.1"
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a putative protein kinase
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                      Tao, W., Zhang, S., Turenchalk, G.S., Chen, W. and Xu, T.
                                                                                                                                                                                                                                                                 suppressor modulates CDC2 activity Nat. Genet. 21 (2), 177-181 (1999) 99140767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumours and pituitary dysfunction
Nat. Genet. '21 (2), 182-186 (1999)
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/organism="Homo sapiens"
/db_xref="taxon:9606".
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/dev_stage="fetus"
1. .4307
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                                                            GTCAGTAGCCGGCAAATGTTACAAGAAATTCGGGAATCCCTTAGGAATTTATCTAAACCA
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AGTCCTGGGGACTTCCTTGAAGGATCATTTTCACTTTTGCTCAGAAGAAAGCTCTGGATC
                                               183 TATCAAATAAAGAAGTCCTTCGTGTGGGCTACATATATAGATGTTTTCATGAAGAGGAGT
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Oy Db	1263	CCTGGAATGCAGAATGGTACTGGACAAACTGATTTCATGATACACCAAAATGTTGTCCCT 1322 	
oy Ob	1323	GCTGGCACTGTGAATCGGCAGCCACCTCCATATCCTCTGACAGCAGCTAATGGACAA 1382 	
, dg	1383	AGCCCTTCTGCTTTACAAACAGGGGATCTGCTGCTCCTTCGTCATATACAAATGGAAGT 1442 	
Qy Dp	1443	AFTCCTCAGTCTATGATGGTGCCAAACAGAAATAGTCATAACATGGAACTATATAACATT 1502 	
Qy Dp	1503	AGTGTACCTGGACTGCAAACAAATTGGCCTCAGTCATCTTCTGCTCCAGCCCAGTCATCC 1562 	
O.y. GD	1563	CCGAGCAGTGGGCATGAAATCCCTACATGGCAACCTAACATACCAGTGAGGTCAAATTCT 1622 	
Q <sub>y</sub>	1623	TTTAATAACCCATTAGGAAATAGAGCAAGTCACTGCTAATTCTCAGCCTTCTGCTACA 1682 	
Oy Dp	1683	ACAGTCACTGCAATTACACCAGCTCCTATTCAACAGCCTGTGAAAAGTATGCGTGTATTA 1742 	
Q <sub>y</sub>	1743	AAACCAGAGCTACAGACTGCTTTAGCACCTACACACCCTTCTTGGATACCACGCCAATT 1802 	
Oy Db	1803	CAAACTGTTCAACCCAGTCCTTTTCCTGAGGAACCGCTTCAAATGTGACTGTGATGCCA: 1862 	
Oy Dp	1863	CCTGTTGCTGAAGCTCCAAACTATCAAGGACCACCACCCTACCCAAAACATCTGCTG 1922 	
Oy Db	1923	CACCAAAACCCATCTGTTCCTCCATACGAGTCAATCAGTAAGCCTAGCAAAGAGGATCAG 1982 	
	1983	CCAAGCTTGCCCAAGGAAGATGAGAGTGAAAGAGTTATGAAAATGTTGATAGTGGGGAT 2042 	
Qy Db	2043	aaagaaaagaaacagattacaacttcacctattactgttaggaaaaacaagaaaga	
Oy Dp	2103	GAGCGAAGGAATCTCGTATTCAAAGTTATTCTCCTCAAGCATTTAAATTCTTTATGAG 2162 	
Oy Dp	2163 (2481	CAACATGTAGAAAATGTACTCAAATCTCATCAGCAGCGTCTACATCGTAAAAAACAATTA 2222 	
oy D	2223 (	GAGAATGAATGATGCGGGTTGGATTATCTCAAGATGCCCAGGATCAAATGAGAAGATG 2282 	

	Qy	2283	CTTTGCCAAAAAGAATCTAATTACATCGTCTTAAAAGGGCTAAAATGGACAAGTCTATG 2342 
	δy	2343	AAGATAAAGACACTAGGAATAGGAGATTTGGTGAAGTCTGTCT
	qq	2661	tigtgaagataaagacactaggaataggagcatttggtgaagtctgtct
	QV Dp	2403	GTAGATACTAAGGCTTTGTATGCAACAAAAACTCTTCGAAAGAAGATGTTCTTCGA.2462 
	Qy	4	CAAGTCGCTCATGTTAAGGCTGAGAGATATCCTGGCTGAAGCTGACAATGAATG
	qq	2781	α
	Qy Dp	2523	GTAGTTCGTCTATATTATTCATTCCAGATAAGGACAATTTATACTTTGTAATGGACTAC 2582 
	Qy	2583	GGGGTGATATGATGAGCCTATTAATTAGAATGGGCATCTTTCCAGAAAGTCT
	qq	2901	
	oy d	. 2643	GCACGATTCTACATAGCAGAACTTACCTGTGCAGTTGAAAGTGTTCAFAAAATGGGTTTT 2702
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	ΟŊ	2763	TGACTTTGGCCTCTGCACTGGCTTCAGATGGACACACGATTCTAAGTACTATCAGAGT 28
•	QQ	3081	ACTGACTTTGGCCTCTGCACTGGCTTCAGATGGACACACGATTCTAAGTACTATCAGAGT 3140
	δ δ	82	FACCATGGATTCAGTAATGAATGGGGGGATCCCTCAAGC 288
	a a	14	GIGACCAICCACGGCAAGAIAGCAIGGAIITCAGIAAIGAAIGGGGGGAICCCICAAGC 320
	Q Q	2883	TICCGATGTGGAGACTGAAGCCATTAGAGCGGAGAGCTGCACGCCAGCCA
	δy	2943	GTCTAGCACATTCTTTGGTTGGGACTCCCAATTATATTGCACCTGAAGTGTTGCTA
	qq	3261	
	δλ	3003	TTGTGTGATTGGTGGTGTTATTCTTTTGAAATGTTG 306
	qq	3321	CAGGATACACACAGTTGTGTGATTGGTGGAGTGTTGGTGTTATTCTTTTTGAATGTTG 338
	δ d	3063	GCACAAACACCATTAGAAACACAAATGAA 
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	b oy	3441	TCTCTTCACATTCCACCACAACTTAACTTCAGTCCTGAACGTTCTGATCTT 11
	δy	3183	PATTAAACTTTGCCGAGGACCCGAAGATCGCTTAGGCAAGAATGGTGCTGATGAAAT
	qq	3501	
	δλ	3243	AGCTCATCCATTTTTAAAACAATTGACTTCTCCAGTGACCT
	QQ	3561	GCTCATCCATTTTTTAAAACAATTGACTTCTCCAGTGACCTGAGACAGCAGCATCTGC
	ò á	3303	CATCAAATTTTGATCCTG
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Marumoto, T.,

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QTALAPTHPSWIPQPIQTVQPSPFPEGTASNVTVMPEVAEAPNYOGPPPPYPKHLLHQ
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sdaakaehingkmstedprqvrnppkfgthhkaloeirnsllpfanetnssrstsbyn
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                                                                Submitted (30-JUN-1999) Tumor Genetics and Biology, Kumamoto University School of Medicine, 2-2-1 Honjo, Kumamoto 860-0811,
                                                                                                                                                                                                                                                                       /note="similar to Drosophila waits tumor suppressor;
localized on mitotic apparatus, specifically
phosphorylated at mitotic checkpoint"
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884 c 817 g 1156 t
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3 (bases 1 to 4241)
Nishiyama, Y., Hirota, T., Morisaki, T., Hara, T., Marum Inda, S., Makino, K., Nakamura, H., Koga, H. and Saya, H. Direct Submission.
                                                                                                                                                                                                                                                                                                                                                /product="WARPTS protein kinase"
/protein_id="AAD50272.1"
/db_xref="G1:5738136"
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Pred. No. 0;
                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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Kishimoto, T., Niwa, S.-i., Nagamine, Y., Nishiyama, Y. and Saya, H. WARTS protein, polynucleotide encoding the same, antisense polynucleotide thereof, and antibody recognizing the protein Patent: Japan (PCT/J998/03739) 24-AUG-1998; Sumitomo Electric Industries, Ltd.; I Taya-cho, Sakae-ku,
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Homo sapiens WARTS protein kinase (WARTS) MRNA, complete cds.
AF164041
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Xu.T., Tao,W., Wang,W., Zhang,S. an
Nucleotide sequences of lats genes
Patent: US 6359193-A 5 19-MAR-2002;
Location/Qualifiers Score 2483; Pred. No. 0; 807 3213 bp US 6359193. /organism="unknown" 764 c 696 g ; patent GI:20252344 62.3%; llarity 87.4%; Conservative .3213 from Unclassified. AR201456 Sequence 5 f AR201456 Similarity 3787 ๙ 946 Unknown Unknown TTTTTT. Query Match Best Local Simmatches 2769; source BASE COUNT 972 1032 1092 DEFINITION ACCESSION VERSION ORGANISM REFERENCE AUTHORS TITLE 852 912 241 301 361 11:52 421 3721 3858 3661 3918 3978 3798 3601· JOURNAL RESULT 4 AR201456 LOCUS KEYWORDS FEATURES ORIGIN SOURCE g δ g g QY q δy g ŏ ŏ Q Pb Qγ g ò QQ q δŏ g δy δ q δy

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Oy Dp	1212	CAACCCAȚCATCATGCAGAGTTCTAGCAAATTTAACTTTCCATCAGGAGACCTGGAATG 1271		
Qy Db	1272	CAGAATGGTACTGGACAAACTGATTTCATGATACACCAAAATGTTGTCCCTGCTGGCACT 1331 		
Q.y D.b	1332 598	GTGAATGGGCAGCCACCACCTCGATATCCTCTGACAGCAGCTAATGGACAAAGCCCTTCT 1391 	. :	
Oy Db	1392 658	GCTTTACAAACAGGGGATCTGCTGCTCCTCGTCATACAAATGGAAGTATTCCTCAG 1451 		
Qy Db	1452 718	H - H		
Oy Dp	1512	GGACTGCAAACAAATTGGCCTCAGTCATCTTCTGCTCCAGCCCGGTCATCCCCGAGCAGT 1571 	<b>6</b> .	
Oy Dp	1572 838	GGGCATGAAATCCCTACATGGCAACCTAACATACCAGTGAGGTCAAATTCTTTTAATAAC 1631 		
Oy Dp	1632 898	CCATTAGGAAATAGAGCAAGTCACTCTGCTAATTCTCAGCTTCTGCTACAACAGTCACT 1691 		
oy Ob	1692 958	GCAATTACACCAGCTCCTATTCAACAGCCTGTGAAAAGTATGCGTGTATTAAAACCAGAG 1751 	7	
oy Db	1752 1018	CTACAGACTGCTTTAGCACCTACACCCTTCTTGGATACCACAGCCAATTCAAACTGTT 1811 		
oy Oy	1812	CAACCCAGTCCTTTTCCTGAGGGAACCGCTTCAAATGTGACTGTGATGCCACTGTTGCT 1871 		
Q.y	1872 1138	GAAGCTCCAAACTATCAAGGACCACCACCACCCTACCCAAAACATCTGCTGCACCAAAAC 1931 		
oy Op	1932 1198	CCATCTGTTCCTCCATACGAGTCAATCAGTAAGCCTAGCAAGAGGATCAGCCAAGCTTG 1991 		
λ g g	1992 1258	CCCAAGGAAGATGAGAGTGAAAAGAGTTATGAAAATGTTGATAGTGGGGATAAAGAAAG 2 		
Qy Op	2052	AAACAGATTACAACTTCACCTATTACTGTTAGGAAAAACAAGAAAGA		
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oy Db	2172	GAAAATGTACTCAAATCTCATCAGCAGCGTCTACATCGTAAAAAACAATTAGAGAATGAA 2231 	•	
Oy Op	23 49			
λά	2292	AAAGAATCTAATTACATCGTCTTAAAAGGGCTAAAATGGACAAGTCTATGTTTGTGAAG 2351		

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2638 TGGAGCGATGGCAGGGAGGAAAATATCAGTGACACTCTGAGCGGATGGTATAAAAT 2697
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                                                                           GTATATGTTTAACACACTAGTAAATAAATGTAATGAGGATTTGTAAAAAGGGCCTGAAATG
                                        2698 GGGAAGCACCCCGAGCACGCTTTCTATGAGTTCACCTTTCGGAGGTTTTTTGATGACAT
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Identifying tumor suppressors in genetic mosaics:
lats gene encodes a putative protein kinase
Development 121 (4), 1053-1063 (1995)
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Chen,W. and Xu,T.
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Submitted (04-NOV-1998) Genetics, HHMI, Yale
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 3213)
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Pred. No. 0;
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                                                              /organism="Mus musculus'/db_xref="taxon:10090"
                                                                                                    /tissue_type="brain"-
/dev_stage="newborn"
<1. .3213
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                        Cocation/Qualifiers
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C (12N15/09, PC C12R1:91) (C12P21/02,C12R1:19),C12N15/00, PC C12R1:91) (C12R1:91) (C12R
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                       GGAAAGCATCCTGAACATGCATTCTATGAATTTACCTTCCGAAGGTTTTTTGATGACAAT
                                            2698 GGGAGCACCCCGAGCACGCTTTCTATGAGTTCACCTTTCGGAGGTTTTTTGATGACAT
                                                                                                               GGCTACCCATATAATTATCCGAAGCCTATTGAATATGAATACATTAATTCACAAGGCTCA
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                                                                                                                               61 GAGGGCTATCCTCCACCACCACCACCACCACCCCCATGAATCCTCCTAATCAAGGACAG
                                                                                                                                                                         AGAGGCATTAGTTCTGTTGGCAGACAACCAATCATCATGCAGAGTTCTAGCAAA
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                                                                                    1 TCTGGAAACATGGAATACGTAATCTCCCGAATCTCTCCTGTCCCACCTGGGGCATGGCAA
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CAA 2141         	CGT 2201     CGT 1140	GCC 2261 	AGG 2321. 111 AGG 1260	GGT 2381     	CGA 2441	CTG 2501     . CTG 1440	AAT 2561     AAT 1500	ATG 2621     ATG 1560	SAA 268     	GAT 2741      GAT 1680	CAC 2801      CAC 1740	AAT 2861 .        AAT 1800	AGA 2921         	.298	3GT 3041     3GT 1980	SAA 3101     	CTC 3161
2 AGGAAAAACAAGAAAGATGAAGAGCGAAGGGAATCTCGTATTCAAAGTTATTCTCCTCR 	2 GCATTTÀAATTCTTTATGGAGCAACATGTAGAAAATGTACTCAAAATCTCATCAGGGCACC 	2 CTACATCGTAAAAAACAATTAGAGAATGAAATGATGCGGGTTGGATTATCTCAAGATG 	2 CAGGATCAAATGAGAAGATGCTTTGCCAAAAGAATCTAATTACATCGTCTTAAAAC 	2 GCTAAAATGGACAAGTCTATGTTGTGAAGATAAAGACACTAGGAATAGGAGCATTTG 	2 GAAGTCTGTCGAAGAAAAGTAGATACTAAGGCTTTGTATGCAACAAAACTCTTCT 	2 AAGAAAGATGTTCTTCTTCGAAATCAAGTCGCTCATGTTAAGGCTGAGAGAGA	2 GCTGAAGCTGACAATGAATGGGTAGTTCGTCTATATTATTCATTC	2 TTATACTITGTAATGGACTACATTCCTGGGGGTGATATGATGAGCCTATTAATTA	2 GGCATCTTTCCAGAAAGTCTGGCACGATTCTACATAGCAGAACTTACCTGTGCAGTTG 	2 AGTGTTCATAAAATGGGTTTTATTCATAGACATATTAAACCTGATAATATTTGATTG 	2 CGTGATGGTCATATTAAATTGACTGACTTTGGCCTCTGCACTGGCTTCAGATGGACACAC 	2 GATTCTAAGTACTATCAGAGTGGTGACCATCCACGGGAAGATAGCATGGATTTCAGTAAT 	2 GAATGGGGGGATCCCTCAAGCTGTCGATGTGGAGACAGAC	2 GCTGCACGCCAGCACCAGCGATGTCTAGCACATTCTTTGGTTGG	2 GCACCTGAAGTGTTGCTACGAACAGGATACACACAGTTGTGTGATTGGTGGAGTGTTGGT 	2 GTTATICTTTTGAAATGTTGGTGGACAACCTCCTTTCTTGGCACAACACCTTTGGAA	2 ACACAAATGAAGGTTATCAACTGGCAAACATCTCTTCACATTCCACCACAAGCTAAACTC
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variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human echromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80146 bp DNA linear PRI 23-JUN-2001 sequence from clone RPI-203A15 on chromosome 6, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (23-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Jun 25, 2001 Lhis sequence version replaced gi:14133045. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the
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Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                              2101 AGTCCTGAAGCTTCTGATCTTATTATTAAACTTTGCCGAGGACCGGAAGATCGCTTGGC
                                                                                                        GACCTGAGACAGCAGTCTGCTTCATACATTCCTAAAATCACACCCGAACAGATACATCA
                                                                              AAGAATGGTGCTGATGAAATAAAAGCTCATCCATTTTTTAAAACAATTGACTTCTCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ote="HUERS-P3 repeat: matches 4954. .5120 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           te="HUERS-P3 repeat: matches 4691. .4762 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .4942 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ote="HUERS-P3 repeat: matches 6797. .7185 of consensus"
   sequence.
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363. .14255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="LIPBa repeat: matches 1590. 1958 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .4703 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                         .uSg/x repeat: matches 145. .297 of consensus"
                                                                                                                                                       rolone_lib="RPCI-1"
11. 153
rnote="LIMC5 repeat: matches 7790. .7931 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58. 8921 atches -677. -198 of consensus" ote="L1M2 repeat: matches -677. -198 of consensus"
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note="AluJb repeat: matches 210. .306 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ucte="AluSp repeat: matches 1. .301 of consensus" 1290. .12343
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                                                                                                                                                                                                                       note="L2 repeat: matches 2234. 2359 of consensus"
135. 2886
                                                                                                                                                                                                                                                                                                                                                                         repeat: matches 2264. .2750 of consensus"
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   The true left end of clone RP1-317N9 is at 78147 in this The true right end of clone RP11-703H16 is at 2000 in this sequence.
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ote="HUERS-P3 repeat: matches 4568.
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ote="AluJo/FRAM repeat: matches 202. .287 of consensus" MEc repeat: matches 2353. 2196 of consensus" 1119 of consensus" 122. .17029 ote="Linada repeat: matches 5319...6300 of consensus" 060. .17261 repeat: matches 5699. .5778 of consensus 378 .23453 lote="MERSA repeat: matches 108. .185 of consensus" 2 repeat: matches 2203. .2267 of consensus" 8320 te="FLAM\_C repeat: matches 2. .125 of consensus" 559. .24859 .305 of consensus" repeat: matches 1. .305 of consensus" repeat: matches 1. .293 of consensus" repeat: matches 1. .302 of consensus" repeat; matches 1. .312 of consensus" ote="Alusg repeat: matches 1. .298 of consensus" .292 of consensus" % repeat: matches 1. .299 of consensus"  $17\,$ .105 of consensus" uSp repeat: matches 34. .303 of consensus" 9117 ote="AluSq repeat: matches 1. 306 of consensus" 1588. 19843 repeat: matches 7. .176 of consensus" .294 of consensus repeat: matches 1. .300 of consensus" R3 repeat: matches 2. .209 of consensus" 5249 ote="Alusg repeat: matches 1. .296 of consensus" 966. .18263 R repeat: matches 41. .241 of consensus" 9557 .160 of consensus" repeat: matches 1. .298 of consensus" te="Alusg/x repeat: matches 89. .310 of uSc repeat; matches 118, .290 of . 5572 te="FRAM/FAM repeat: matches 4...72 of copies 2 mer ta 100% conserved" 7549 conserved" .5331 080. .17261 ote="MBR74A repeat: matches 1. .171 of 490. .17788 ote="Alusx repeat: matches 1. .309 of MA4A repeat: matches 3603. ote="FLAM\_C'repeat: matches 1.076. .16112 matches 12. luSc repeat: matches 1. lusx repeat: matches 1. copies 2 mer ta 100% 8818 note="Alu repeat: matches 79. 5122. .17029' cc 648 =not\_experimental copies 2 mer te="AluJo repeat: 71. 21270 /note="AluSq.30581. note="Alusa lote="Al

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/note="LIM1 repeat: matches 1407.
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/note="MITIF repeat: matches 100.
32688. .32820
/note="FLAM_C repeat: matches 1.
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/note="L1MEc repeat:
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Toshihiko,K., Shinichiro,T., Kyoko,N., Yasuyuki,N. and Hideyuk warts Protein, polynucleotide encoding the protein, antisense polynucleotide thereof and antibody recognizing the protein Patent: JP 1999089580-A 2 06-APR-1999;
SUMITOMO ELECTRIC IND LTD
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G01N33/5522/702,C12P21/02,
PC (C12N15/09,C12R1:91),(C12P21/02,C12R1:19),C12N15/00,
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                                                                                                        Length 1374;
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                                  1. .1374
/organism='Unidentified'
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                                                                                                         Score 1360.4; DB 6;
Pred. No. 6.3e-290;
); Mismatches 1;
                           Location/Qualifiers
                                                                                  392
                                                           1. .1374
/organism="unidentified"
                                                                          /db_xref="taxon:32644"
252 c 288 g
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Strandedness: Double;
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                   Topology: Linear;
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ilarity 99.9%;
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Department of Experimental Hematology, Institute of Radiation Medicine,
Beijing Taiping Road 27, Beijing, Beijing 100850, P. R. China
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Eutheria; Primates; Catarrhín; Hominidae; Homo.
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                                                                                                                       /protein_id="AAF69600.1"
/protein_id="MADKLSDRYFKASYTFQEVHYFIQGLFEGLEMAGLQQVPEVQNLS
DWFFIMCLVDHALAQSEVCYRQVGEGLEGORGLKEGWYRLVQLDGSQVGFQJIG
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                                                                                                                                                                                           BP; '452 A; 440 C; 451 G; 464 T; 0 other;
                                                                                                       /note="predicted protein of H01474"
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                                                                                                                                                                                                            Score 930.8; DB 17;
Pred. No. 5.6e-195;
0; Mismatches 2;
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/tissue_type="liver"
/dev_stage="fetus"
complement(841. .1530)
                           /db_xref="taxon:9606"
 Location/Qualifiers
                                                                                     /codon_start=1
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S Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Paro, S., Ferreira, P., FitzHugh, W., Galagan, J., Garad-Pierre, N., Ferreira, P., FitzHugh, W., Galagan, J., Garad-Pierre, N., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McRernan, K., McPheters, R., Talu, G., Norman, C., Raymond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R., Shander, S., Sevetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Strauer, S., Sevetti, M., Roy, A., Santos, R., Sauder, S., Theodore, J., Viel, R., Tavers, M., Travis, N., Trigillo, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Shahaiter, A., Zambek, L., Zimmer, A. and Zody, M., Submassion.
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Mus musculus clone RP24-258P4, WORKING DRAFT SEQUENCE, 17 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Coollymore, A., Cooke, P., Darrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gradam, E., Grand-Plerre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Grand-Plerre, N., Hagos, B., Karatas, A., Kalls, C., Macdonald, P., Major, Y., Madora, C., Macdonald, P., Major, J., Malnay, C., Macdonald, P., Major, J., Malpaga, V., Murphy, T., Maylor, J., Wheneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Worbu, C., Norman, O. Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
782
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                                                                                                                                                                                                                                                                                                                                     902
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                                            214 CCAGGGAATGTGCAGCAATCAGTTAACCGCAAACAGAGCTGGAAAGGTTCTAAAGAATCC
                                                                                                                                                                                                                                                                                                                                                                             94 CCCAACTCACAGACAGATGTAGGAAGACCTTTGTCTGGATCTGGTATATCAGCATTTGTT
CCAGGGAATGTGCAGCAATCAGTTAACCGCAAACAGAGCTGGAAAGGTTCTAAAGAATCC
                                                                                                                                                              TTAGTTCCTCAGAGGCATGGCCCGCCACTAGGAGAAAGTGTGGCCTATCATTCTGAGAGT
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AC102712.2 GI:22381704
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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Mus musculus, clone RP24-258P4
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Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schubback, R., Seamann, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J. Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Zeinbek, L., Zimmer, A. and Zody, M., Wyman, D., Young, G., Zainoun, J., Direct Submission
                                                                                                                                      Submitted (21-A0G-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 21, 2002 this sequence Version replaced g1:17060822.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert size: 176000; agarose-fp
Insert size: 162890; sum-of-contigs
Quality coverage: 7.2 in Q20 bases; agarose-fp
Quality coverage: 7.8 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: Plasmid; n/a; 100% of reads
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
                                                                                                                                                                                                                                            http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
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control of 15046 bp in length

ap of 100 bp

control of 18800 bp in length
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16508 bp in length
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f 1268 bp in length
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f 3274 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 bp
f 2926 bp in length
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f 1085 bp in length
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36805: conti
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3531: co
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11116: co
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8090:
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Pred. No. 1e-176;
0; Mismatches 141; Indels
164490: contig of 4286 bp in length.
                                                                                              /clone_1rb24-258P4"
/clone_1rb="RPCI-24 Male Mouse
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35286 c 34742 g 45505 t
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0952. .85997
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note="assembly_fragment"
                                                            /organism="Mus musculus"
                                                                             /db_xref="taxon:10090"
                       Location/Qualifiers
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Best Local Similarity 86.8%;
Matches 957; Conservative (
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//Organism="unidentified"
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Toshhiko,K., Shinichiro,T., Kyoko,N., Yasuyuki,N. and Hideyuki,S. Toshhiko,F., Shinichiro,T., Kyoko,N., Yasuyuki,N. and Hideyuki,S. warts Protein, polynucleotide encoding the protein antisense polynucleotide thereof and antibody recognizing the protein Patent: JP 1999089580-A 4 06-APR-1999;
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             TATTCATTCCAAGATAAAGGACAATTTATACTTTGTAATGGACTACATTCCTGGGGGTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Structure, expression, and chromosome mapping of LATS2, a mammalian homologue of the Drosophila tumor suppressor gene lats/warts Genomics 63 (2), 263-270 (2000)
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HKMGFIHRDIRPDNILIDLDGHIKLTDFGLCTGFRWTHNSKYYQKGNHMRQDSMEPGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                 CATCCTGAACATGCATTCTATGAATTTACCTTCCGAAGGTTTTTTGATGACAATGGCTAC 3497
ATCACACACCCAACAGATACATCAAATTTTGATCCTGTTGATCCTGATAAATTATGGAGT 3377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yabuta, N., Fujii, T., Copeland, N.G., Gilbert, D.J., Jenkins, N.A., Nishiguchi, H., Endo, Y., Toji, S., Tanaka, H., Nishimune, Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (22-FEB-1999) Hiroshi Nojima, Research Institute for
Microbial Diseases, Osaka University, Department of Molecular
Genetics; Yamadaoka 3-1, Suita, Osaka 565-0871, Japan
(E-mall:hnojima@biken.osaka-u.ac.jp, Tel:81-6-6875-3980,
Pax:81-6-6875-5192)
                       'product="warts/lats-like kinase"
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db_xref="taxon:10090"
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Location/Qualifiers
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/gene="MmLATS2"
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 TATTCATTCCAAGATAAGGACAATTTATACTTTGTAATGGACTACATTCCTGGGGGTGAT
                                   ATGATGAGCCTATTAATTAGAATGGGCATCTTTCCAGAAAGTCTGGCACGATTCTACATA
                                                                                                      AAACCTGATAATATTTTGATTGATCGTGATGGTCATATTAAATTGACTTTTGGCCTC
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PAT 31-JAN-2002

linear

DNA

dq 5486

E38226 5486 Human tumor regulatory gene.

LOCUS DEFINITION

RESULT 14 E38226

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C12N15/09,A61K31/00,A61K38/27,C07K14/47,C07K14/525,C12Q1/68, PC
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                                                                Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo
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Pred. No. 9.1e-154;
0; Mismatches 556;
                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .5486
                                                                                                              Koga,J., Kono,K. and N.2.F.
Human tumor regulatory gene
Patent: JP 2000210086-A 1 02-AUG-2000;
NIHON CHEMICAL RESEARCH K K
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PC A61K37/36, (C12N15/00, C12R1:91)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
1452 c 1390 g 1266
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                                                                   Chordata;
                                                                                   Primates;
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JP 2000210086-A/1
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Conservative (
 GI:18626935
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                                                                     Eukaryota; Metazoa;
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E38226.1 GI:18626
JP 2000210086-A/1.
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                                 Homo sapiens.
Homo sapiens
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SOURCE
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AUTHORS
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E38227
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1462 ACCTCGCCAATAACAAGCATCCTGAGCACGATTTAACGAATTCACCTTCCGAAGGTTC 3521
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                                                                     2625 TACATCCCTGGTGGGGACATGATGAGCCTGCTGATCCGGATGGAGGTCTTCCCTGAGCAC
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         2685 CTGGCCCGGTTCTACATCGCAGAGCTGACTTTGCCCATTGAGAGTGTCCACAAGATGGC
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                               2445 AAGGTGGACACTCACGCCTGTACGCCATGAAGACCCTAAGGAAAAAGGATGTCCTGAAC
                                                                                                                                                    2580 TACATTCCTGGGGGTGATATGATGAGCCTATTAATTAGAATGGGCATCTTTCCAGAAAGT
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EUKATYOCA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 5486)

I (bases 1 to 5486)

K Koga,J., Kono,K. and N,Z.F.

Human tumor regulatory gene

L Patent: JP 2000210086-A 2 02-AUG-2000;

NIHON CHEMICAL RESEARCH K K

OS Homo sapiens (human)

PD 02-AUG-2000

PP 1000210086-A/2

PP 25-JAN-1999 JP 1999016223

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3480 TTTGATGACAATGGCTACCCATATAATTATCCGAAGCCTATTGAATATGAATACATTAAT 3539
                                           3522 TTTGATGACAATGGCTACCCTTTCGATGCCCAAAGCCTTCAGGAGCATCACAG 3581
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Pred. No. 9.1e-154;
0; Mismatches 556;
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1. 5486
/ Organism="Homo sapiens"
/db_xref="taxon:9606"
a 1451 c 1388 g 1267
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E38227.1 GI:18626936
JP 2000210086-A/2.
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Best Local Similarity 66.3%;
Matches 1123; Conservative
                                                                                                                                                                                                                 3582 GCTGAGAGCTCAGA 3595
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3224 2984 TTGGTGGGACAACCTCCTTTCTTGGCACAAACACCTTAGAAACACAAATGAAGGTTATC .3119 2639 5698 2804 2939 2940 CGAÜGTCIAGCACAITCIIIGGIIGGGACICCCAAITAIATTICCACCIGAAGIGIIGCIA 2999 2985 AGGIGCCTGGCATTCACTGGTGGGGACTCCAAACTACATCGCACCCGAGGTGCTCCTC 3044 AACTGGCAAACATCTTCACATTCCACCACAAGCTAAACTCAGTCCTGAAGCTTCTGAT 3179 CIGAAGGCCCACCCTTCTTCAGCGCCATTGACTTCTCCAGTGACATCCGGAAGCAGCAGCA 3344 2399 2459 2579 2684 GAGCAGCACGTGGAGAATGTCATCAAAACCTACCAGCAGAAGGTTAACCGGAGGCTGCAG 2264 CTTATTATTAAACTTTGCCGAGGACCCGAAGATCGCTTAGGCAAGAATGGTGCTGATGAA ATAAAAGCTCATCCATTTTTTAAAACAATTGACTTCTCCAGTGACCTGAGACAGCAGTCT TACATCCCTGGTGGGGACATGATGAGCCTGCTGATCCGGATGGAGGTCTTCCCTGAGGAC 2805 CTCACAGATTTCGGCCTCTGCACTGGGTTCAGGTGGACTCACAATTTCAAGGTTACCAG AGCTGTCGATGTGGAGACAGACTGAAGCCATTAGAGCGGAGAGCTGCACGCCAGCACCAG TACATTCCTGGGGGTGATATGATGAGCCTATTAAATTAGAATGGGCATCTTTCCAGAAAGT 2760 TIGACTGACTITGGCCTCTGCACTGGCTTCAGATGGACACACGATTCTAAGTACTATCAG ATGITIGIGAAGATAAAGACACTAGGAATAGGAGCATTIGGIGAAGTCTGTCTAGCAAGA CGAAATCAAGTCGCTCATGTTAAGGCTGAGAGATATCCTGGCTGAAGCTGACAATGAA TGGGTAGTTCGTCTATATTCATTCCAAGATAAGGACAATTTATACTTTGTAATGGAC CTGGCACGATTCTACATAGCAGAACTTACCTGTGCAGTTGAAAGTGTTCATAAAATGGGT 2700 TITATICATAGAGATATIAAACCIGATAATATITIGATIGATCGIGAIGGICATAITAAA CTGGAGCAAGAATGGCCAAAGCTGGACTCTGTGAAGCTGAGCAGGAGCAGATGCGGAAG ATGCTTTGCCAAAAGAATCTAATTACATCCTCTTAAAAGGGCTAAAATGGACAAGTCT **TTAGAGAATGAAATGATGCGGGTTGGATTATCTCAAGATGCCCCAGGATCAAATGAAAAG** 2880 3045 3105 3165 3180 3225 3240 3285 2865 2925 3000 3060 3120 2640 2820 2385 2445 2460 2505 2520 2565 2625 2685 2745 2205 2220 2265 2280 2325 2340 2400 2580 g G qq ò g ð g ò g δ g ò g ò à g ð g ò g ò g -g g ò 음 ð g ò g õ

3419 3539 3359 3404 3405 GAAGAAAGCCCTTGGAAGGCAGC---GAAGGTAGCACGCAGGCCTGGGACACTC 3462-ACCTGGCCAATAACAAGCATCTGAGGATTTTACGAATTCACCTTCGAAGGTTC 3480 ITTGATGACAATGGCTACCCATATAATTATCCGAAGCCTATTGAATATGAATAAAT 3345 GCCCCCTACGTTCCCACCATCGACCCCTGGACACCTCGAATTTCGACCCCTAGAT CCTGATAAATTATGGAGTGATGATAACGAGGAAGAAAATGTAAATGACACTCTCAATGGA 3300 GCTTCATACATTCCTAAAATCACACACCCAACAGATACATCAAAATTTTGATCCTGTTGAT 3582 GCTGAGAGCTCAGA 3595 3540 TCACAAGGCTCAGA 3553 3360 q g ò ōλ g οχ Qγ

Search completed: January 16, 2003, 18:10:29 Job time: 7470.05 secs Mouse Lats2 (large Human WART2 cDNA. DNA encoding a tum DNA encoding a tum

Human cancer-inhib DNA encoding novel CDNA SS1771 encodi

CDNA SS1771A encod

Human protein tyro Human warts gene f Human TGF-beta rec Lats gene encoding

Drosophila melanog Drosophila melanog cDNA encoding nove DNA encoding novel Disease associated

Tuman colon cancer

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Run on:

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Human; h-lats gene; large tumour suppressor; fetal brain; protein-serine/threonine-kinase; cell proliferation; antisense; dominant-negative; cancer; degenerative disorder; trauma; growth deficiency; therapy; antitumour; vulnerary; diagnostic; transgenic plant; transgenic animal; growth; senescence; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H-lats gene encoding large tumour suppressor.
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231.3623
/*tag= a
/product= Lats protein
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AAZ61160
AAI71765
ABK43457
AAZ61158
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Human WART1 cDNA.
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1 acctttgggttgctgggacg.....agagtttttgaaattttttt 3984
                                                                                       January 16, 2003, 09:50:07; Search time 508.163 Seconds
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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Listing first 45 summaries
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Database :

Searched:

Human immune/haema DNA encoding novel Drosophila melanog A. gossypii AG007

95US-0411111 96WO-US04101

27-MAR-1995; ·

26-MAR-1996;

Mouse Lats' (large M-lats gene encodi

protei gene f

Human warts warts

Human Human

AAX32982 ABA08740 AAX32984

2422 1360.4 1233.2 788.6

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Orosophila melanog

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This sequence encodes a human large tumour suppressor h-lats protein, and has been isolated from a fetal human brain phage lambda-gtl0 cDNA library using a 2.1-kb DNA probe from the mouse m-lats gene (AAT42119). The full-length cDNA is present in plasmid pBS(KS)-h-lats. The gene encodes a putative protein-serine/threonine-kinase, and inhibits cell proliferation and plays a crucial role throughout development. Activators or inhibitors of lats function (e.g. an antisense oligonucleotide or dominant-negative lats fragment) may be used in therapy of cancer or other proliferative disorders,
                                                                                                                                                                                                                                                                                                                                                                                                          degenerative disorders, trauma, growth deficiency, etc., and fragments of the gene may be used as diagnostic probes. A lats-inhibitor sequence may be expressed in a transgenic plant or
                                                                                                                      New isolated large tumour suppressor gene – used to develop prod for inhibiting cell proliferation or for enhancing proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to confer increased growth and inhibit senescence
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                                                                                                                                                                                  Claim 6; Page 118-123; 215pp; English
                       Zhang
                     Yu W,
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                                                             WPI; 1996-455275/45
                                                                              P-PSDB; AAW05178
                     Wang W,
                     Tao W,
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Sequence 3984 BP; 1280 A; 847 C; 798 G; 1059 T; 0 other;

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240 ACAGTCCTGGGGACTTCCTTGAAGGATCATTTTCACTTTTGCTCAGAAGAAAGCTCTGGA 180 TCTATCAAATAAAGAAGTCCTTCGTGGGCTACATATATAGATGTTTTCATGAAGAGGA 240 420 420 CTCTGCTTCCATTTGCAAATGAAACAAATTCTTCTCGGAGTACTTCAGAAGTTAATCCAC ACAGTCCTGGGGACTTCCTTGAAGGATCATTTTCACTTTTGCTCAGAAGAAAGCTCTGGA 180 Gaps 1 ACCTTTGGGTTGCTGGGACGGACTCTGGCCGCCTCAGCGTCCGCCCTCAGGCCCGTGGCC 60 TCTATCAAATAAAGAAGTCCTTCGTGTGGGCTACATATATAGATGTTTTCATGAAGAGA GTGAAAAGCCAGAAGGATATAGACAAATGAGGCCTAAGACCTTTCCTGCCAGTAACTATA CTGTCAGTAGCCGGCAAATGTTACAAGAAATTCGGGAATCCCTTAGGAATTTATCTAAAAC CATCTGATGCTGCTGAGGCTGAGCATAACATGAAAAATGTCAACCGAAGATCCTCGAC AAATGCTTCAAGACTTGCAAGCTGCTGCATTTGATGAGGATATGGTTATACAAGCTCTTC **AAGTCAGAAATCCACCCAAATTTGGGACGCATCATAAAGCCCTTGCAGGAAATTCGAAACT** CTCTGCTTCCATTTGCAAATGAAACAAATTCTTCTGGGAGTACTTCAGAAGTTAATCCAC Score 3984; DB 17; Length 3984; Pred. No. 0; 0; Indels ó; Mismatches ; 0 100.0%; 100.08; Matches 3984; Conservative Similarity Query Match Local 61 61 121 181 241 301 361 361 541 121 181 421 421 481 481 541 301 601 g ç ò g ô g ð g ŏ 엄 à 셤 ð ò

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	δy	661	CGACGAGGAGCAGCTGCAGCAGCTGCCAGACCT	720
٠.	qq	661	ATCCTCGACGAGAGGAGGTGCTGCAGCTGCCAGACCTATTAATGCCAGCATG	
	Qγ	721	AACCAGGGAATGTGCAGCAATCAGTTAACCGCAAACAGAGCTGGAAAGGTTCTAAAGAAT	780
	qq	721	CAGGGAATGTGCAGCAATCAGTTAACCGCAAACAGAGCTGGAAAGGTTCTAAAGAA	780
	οy	781	CCTTAGTTCCTCAGAGGCATGGCCCGCCACTAGGAGAAAGTGTGGCCTATCATTCTGAGA	840
	qq	781	CTTAGTTCCTCAGAGGCATGGCCCGCCACTAGGAGAAAGTGTGGCCTATCATTCTGAG	840
	Qy 4	841	GTCCCAACTCACAGACAGATGTAGGAAGACCTTTGTCTGGATCTGGTATATCAGCATTTG	006
	2	T +0		<b>&gt;</b> '
	oy D	901	TTCAAGCTCACCCTAGCAACGGACAGAGAGTGAACCCCCCCACCACCTCAACTAAGGA TTCAAGCTCACCCTAGCAACGGACAGAGAGAGTGAACCCCCCCC	096
	Οÿ		FTACTCCTCCACCACCTCCAAGAGGCCAGACTCCCCCCTCCAAGAGGTACAAĈ	0
	pp	961	GIGITACTCCTCCACCACCTCCAAGAGGCCAGACTCCCCCCCCC	1020
: ,	Qy	1021	CCCTTCATGGGAACCAAACTCTCAAACAAAGGGCTATTCTGGAAACATGGAATAC	1080
	qq	1021	TCAAACAAAGCGCTATTCTGGAAACAT	1080
	QY	1081	TAATCTCCCGAATCTCTCTGTCCCACCTGGGGCATGGCAAGAGGGCTATCCTCCACCAC	1140
	3 .	,		
	oy Ob	1141	CHCTCAACACTCCCCCATGAACCTCCTAATCAAGAACAAAAAGGCAATGATTCTTTC 	1200
	φ	1201	CTGTTGGCACACAACCAATCATGCAGAGTTCTAGCAAATTTAACTTTCCATCAGGA	.01
	g .	707	CAATCATCAGGAGGTTCTAGCAAATTTAACTTTCC	<b>V</b>
	Oy Dp	1261	TGCAGAATGGTA 	1320 1320
	QΥ	1321	AATCGGCAGC	1380
6	Dp	1321		3
	QY	1381	GGATCTGCTGCTTCGTCATATACAAATGGAA	1440
	QQ	1381	CCTTCTGCTTTACAACAGGGGATCTGCTGCTCCTTCGTC	4
	δy		AACAGAAATAGTCATAACATGGAACTATATAACA	20
	Dp	1441	.AGTCTATGATGGTGCCAAACAGAAATAGTCATAACATGGAACT	1500
	Qy	1501	TIAGIGIACCIGGACIGCAAACAAAITGGCCICAGICAICTICIGCICCAGCCCAGICAI	9
•	<b>අ</b>	1501	TACCTEGACTGCAAACAAATTGGCCTCAGTCATCTTCTGCTCCAGCC	
	δy.	1561	ATGGCAACCTAACATACCAGTGAGGTCAAATT	1620
	qq	1561	cccaagcagragaaarcccaaargaaargaaaaaraaaaaaaa	9
	δλ	Ċ,	CTTTAATAACCCATAGGAAATAGAGCAAGTCACTCTGCTAATTCTCAGCCTTCTGCTA	68
	qq	1621	ACCCATTAGGAAATAGAGCAAGTCACTCTGCTAATTCTCAGCCTTCTGCT	œ
	y d	1681	CÁACAGTCACTGCAATTACACCAGCTCCTATTCAACAGCCTGTGAAAAGTATGCGTGTAT 	1740
	3	0	THI	*

1861   AGCAGGTTGTCCAAACCCCAACAACTACAGGACCACCCCCAAAACACTCCCCCAAAACCTCCCCCCAAAACCTCCCCCAAAACCCCTCCCCCAAAACCCCTCCCCCAAAACCCCTCCCCCAAAACCCCTCCCCCAAAACCCCTCCCCAAAACCCCTCCT
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QQ O	821 GT	SACCATCCACGGCAAGATAGCATGGATTTCAGTAATGAATG	œ
ΟŊ	æ	GTCGATGTGGAGACAGACTGAAGCCATTAGAGCGGAGAGCTGCACGCGGCAGCACCAGC 29	4
qq	881	3TCGATGTGGAGACAGACTGAAGCCATTAGAGCGGAGAGCTGCACGCCAGCACCAGC 29	4
δ å	94	31CTAGCACATTCTTTGGTTGGGACTCCCAATTATATTGCACCTGAAGTGTTGCTAC 30	
Q (	9416	STCTAGCACATTCTTTGGTTGGGACTCCCAATTATATTGCACCTGAAGTGTTGCTAC 30	)
y y	3001 GAAC	AGGATACACACACACTTCTCATTGCTGGTGGTGCTTGCTGTTTATTCTTTTTGAAATGT 30.   IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	ب و
. 0	061 T	GGGGACAACCTCCTTTGGCACAAAACACCTTTTGGAAAGGTTTATCA 31	0
g Q	90		N (4
δō	3121 ACT	SGCAAACATCTCTCACATTCCACCACAAACTCAGTCCTGAAGCTTCTGATC 31	
qq	121	GCAAACATCTCTTCACATTCCACACAAGCTAAACTCAGTCCTGAAGCTTCTGATC 31	8
οy	3181 TTA		240
qq	3181 TTA	ATTAAACTTTGCCGAGGACCCGAAGATCGCTTAGGCAAGAATGGTGCTGATGAAA 32	4
δy	F	CTCCAGTGACCTGAGACAGCAGTCTG 33	Ο,
qq	3241 TAA	SCICAICCAITITIAAAACAAIIGACIICICCAGIGACCIGAGACAGCAGICIG 33	0
ΟŊ	3301 CTT	CATACATTCCTAAAATCACACCCAACAGATACATCAAATTTTGATCCTGTTGATC 33	9
đ,	3301 CTT	CATACATICCTAAAAICACACACCCAACAGATACAICAAAITITIGAICCIGTIGAIC 33	9
Qy	3361 CTG	ATAAATTATGGAGTGATGATAACGAGGAAAATGTAAATGACACTCTCAATGGAT 34	420
QQ	3361 CTG	ataaattatggagtgatgataacgaggaagaaatgtaaatgacactctcaatggat 34	7
Qy	3421 GGT	SCATTCTATGAATTACCTTCCGAAGGTTTT 34	ω
qq	3421 GGT	AAAAATGGAAAGCATCCTGAACATGCATTCTATGAATTTACCTTCCGAAGGTTTT 34	8
Oy	3481 TTG	CATATAATTATCCGAAGCCTATTGAATATGAATACATTAATT 35	540
qq	3481 TTG	SACAATGGCTACCCATATAATTATCCGAAGCCTATTGAATATGAATACATTAATT 35	4
Οy	541 CAC	AAGGCTCAGAGCAGCAGTGGGATGAAGATGATCAAAACACAGGCTCAGAGATTAAAA 36	.009
qa		AAGGCTCAGAGCAGCAGTCGGATGAAGATGATCAAAACACAGGCTCAGAGATTAAAA 36	0
Øγ	3601 ATC	GCGATCTAGTATATGTTTAACACACTAGTAAATAAATGTAATGAGGGATTTGTAAAG 36	099
QQ	3601 Arc	GCGATCTAGTATGTTTTAACACACTAGTAAATAAATGTAATGAGGATTTGTAAAAG 3	099
Οy	3661 GGC	CTGAAATGCGAGGTGTTTTGAGGTTCTGAGAGTAAAATTATGCAAATATGACAGAGC 3	720
Db	61	THE STREET OF TH	720
ΟŸ	3721 TAT	TTTTCTAAATTATGGGAAATCCTTTTAA 3	780
QQ	3721 TAT	ATGTGTGCTCTGTGTACAATATTTTTTTTTTTTTTTTTT	780
δλ	3781 AAT	STTAAITTATTCCAGCCGTTTAAATCAGTATTTAGAAAAAAAATTGTTATAAGGAAAG 3	340
QO	3781 AAT	STTAATTTATTCCAGCCGTTTAAATCAGTATTTAGAAAAAATTGTTATAAGGAAAG 3	340
Οý	3841 TAAAT	RATGAACTGAATATTATAGTCAGTTCTTGGTACTTAAAGTACTTAAAATAAGTAG 3	900
dO .	3841 TAA	TATGAACTGAATATTATAGTCAGTTCTTGGTACTTAAAGTACTTAAAATAAGTAG 3	006
ΟŊ	3901 TGC	CTTTGTTTAAAAGGAGAAACCTGGTATCTATTTGTATATATGCTAAATAATTTTAAAA 396	096

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Length 3984;

DB 21;

Sequence 3984 BP; 1280 A; 847 C; 798 G; 1059 T; 0 other;

Query Match

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Use of lats proteins, complexes of lats and cdc2 for treating cancer that is refractory to treatment by standard chemotherapy and radiation therapy, and disorders associated with aberrant levels of cdc2 activity
                                                                                                                                                                                   Human, Lats; large tumour suppressor; cytostatic; vulnerary; cell overproliferation inhibitor; cdc2; cell cycle-dependent kinase; treatment; prevention; screening; cancer; skin; ovarian tumour; soft tissue sarcoma; pituitary disorder; gene therapy; hyperplasia; lH; luteinizing hormone hypoponadotropic hypoponadism; metaplasia; dysplasia; degenerative disorder; growth deficiency; physical trauma; hypoproliferative disorder; lesion; wound; lats knock-out mouse; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fukumoto RK,
                                                                                                                                                               Human Lats (large tumour suppressor) DNA
                                                                                                                                                                                                                                                                                                                    /product= "Lats protein"
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                                          TACAAGAGTTTTTGAAATTTTTT 3984
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Stewart RA;
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9803-0096997
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P-PSDB; AAY70390.
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Turenchalk GS,
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                                              ACAGTCCTGGGGACTTCCTTGAAGGATCATŤTTCACTTTTGCTCAGAAGAAAGCTCTGGA
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The present sequence is a DNA encoding human Lats (large tumour suppressor) protein which is a cell overproliferation inhibitor and a negative regulator of cell cycle-dependent kinase cdc2/cyclin A. The present sequence is useful for treating cancer that is refractory to standard chemotherapy or radiation therapy such as hyperplasia, metaplasia, or dysplasia, and disorders associated with aberrant levels of cdc2 activity. Conditions treated by promoting cdc2 function include degenerative disorders, growth deficiencies, hypoproliferative disorders, physical trauma, lesions, and wounds. An animal model preferably a mouse, in which a lats gene has been disrupted by homologous

Claim 44; Fig 12; 134pp; English.

recombination, e.g. a lats knock-out mouse, is used for screening compounds that can be used to treat or prevent cancer, particularly skin cancer, soft tissue sarcomas and ovarian tumours, and disorders associated with pituitary dysfunction e.g. luteinizing hormone (LH) hypogonadotropic hypogonadism. The lats DNA is also used in gene therapy.

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S G	1021	CICCCCTTCATGGGAACCAAACTCTCAAACAAGCGCTATTCTGGAAACATGGAATACG CICCCCCTTCATGGGAACCAAACTCTCAAACAAAGGGCTATTCTGGAAACATGGAATACG	1080		
Q <sub>Y</sub>	1081	TAATCICCCGAATCTCTCTGTCCCACCTGGGGATGGCAAGAGGGCTATCCTCCACCAC 1	1140		
Qy Db	1141	ACTTCCCCATGATCCTCCTAATCAAGGACAGAGGGATTAGTTCTGTTC 	1200		
Oy Dp	1201	CTGTTGGCAGACAACCAATGATGCAGAGTTCTAGCAAATTTAACTTTCCATGAGGA 1 	1260	.,	
Oy Dp	1261	GACCTGGATGCAGAATGGTACTGGACAAACTGATTTCATGATACACCAAAATGTTGTCC 1	1320		
Oy Dp	1321	CTGCTGGCACTGTGAATCGGCAGCCACCTCCATATCCTCTGACAGCAGCTAATGGAC 1	1380		
O D D	1381 1381	AAAGCCTTCTGCTTTACAAACAGGGGGATCTGCTGCTCCTTCGTCATATACAAATGGAA 1	1440	٠.	
O.Y D.b	1441	GTATTCCTCAGTCTATGATGGTGCCAAACAGAAATAGTCATAACATGGAACTATATAACA 1	1500	,	
oy D	1501	TTAGTGTACCTGGACTGCAAACAAATTGGCCTCAGTCATCTTCTGCTCCAGCCCAGTCAT 1	1560 1560		
92	1561	CCCCGAGCAGTGGGCATGAATCCCTACATGGCAACCTAACATACCAGTGAGGTCAAATT 1	1620 1620		
OY Db	1621 1621	CTTTTAATAACCCATTAGGAAATAGACAAGTCACTCTGCTAATTCTCAGCTTCTGCTA 1	1680 1680		
Qy Db	1681 1681	CAACAGTCACTGCAATTACACCAGCTCCTATTCAACAGCCTGTGAAAAGTATGCGTGTAT 1	1740		
QY Dp	1741	TAAAACCAGAGCTACAGACTGCTTTAGCACCTACACACCCTTCTTGGATACCACAGCCAA	1800		
O.y	1801	TTCAAACTGTTCAACCCAGTCCTTTTCCTGAGGAACCGCTTCAAATGTGACTGTGATGC 1	1860		
Oy Dp	1861	CACCTGTTGCTGAAGCTCCAAACTATCAAGGACCACCACCACCGTACCCAAAACATCTGC 1	1920 1920		
Oý Op	1921	TGCACCAAAACCCATCTGTTCCTCCATACGAGTCAATCAGTAAGCCTAGCAAAGAGGATC 1	1980		
Qy Dp	1981	AGTGGGG                 AGTGGGG .	2040		
Qy Db	2041	ATAAAGAAAGAAAGGAATTACAACTTCACCTATTACTGTTAGGAAAAAGGAAGAAGGAGG 2 	2100		

y q	2101	AAGAGCGAAGGAATCTCGTATTCAAAGTTATTCTCCTCAAGCATTAAAATTCTTATGG 2160
Oy	Ä	PAACATGTAGAAAATGTACTCAAATCTCATCAGCAGCGTCTACATCGTAAAAACAAT 222
qa .	2161	GCAACATGTAGAAAATGTACTCAAATCTCATCAGCGCGCGTCTACATCGTAAAAAACAAT 222
S 8,	7 (7	GAGAAAGA 228            - GAGAAAGA 228
Qy	28	TACATCGTCTTAAAAGGGTAAAATGGACAAGTCTA 234
අධ	28	GCTTTGCCAAAAAGAATCTAATTACATCCGTCTTAAAAGGGCTAAAATGGACAAGTCTA 234
g Qy	2341	TCTTTGTGAAGATAAAGACACTAGGAATAGGAGCATTTGGTGAAGTCTGTCT
Qy	2401	TACTAAGGCTTTGTATGCAACAAAACTCTTCGAAAGAAAG
ΩD	2401	STAGATACTAAGGCTTTGTATGCAACAAAAACTCTTCGAAAGAAGAAGTGTTCTTCTTC 2
Oy Dp	2461	ATGAAT
, o <sub>y</sub>	2521	CCTATATTATTCATTCCAGATAAGGACAATTTATATACTTTGTAATGGACT 258
<sup>QQ</sup> .		STICGICIATATIATICATICCAAGATAAGGACAATITATACTITGIAATGGACT
Vo 4	2581	GGTGATATGATGAGCCTATTAATTAGAATGGGCATCTTTCCAGAAAGTC 26 
δλ	64	ACGATTCTACATAGCAGAACTTACCTGTGCAGTTGAAAGTGTTCATAAAATGGGTT 270
qq	64	7.0
Οy	2701	CCATAGAGATATTAAACCTGATAATATTTTGATTGATGGTGGTGGTGGTGATTAAAT 2
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연	i (1)	GTGGTGACCATCCACGCAAGATACCATGGATTCAGTAATGAATG
δλ	2881	GGATGTGGAGACACAGACTGAAGCCATTAGAGCGGAGAGCTGCACGCAGCACCAGC 294
QQ	2881	TECACCCAGCACCAGC 294
Qy	2941	AGCACATTCTTTGGTTGGGACTCCCAATTATATTGCACCTGAAGTGTTGCTAC 300
qq	2941	STCTAGCACATTCTTTGGTTGGGACTCCCAATTATATTGCACCTGAAGTGTTGCTAC 800
QY	3001	ACACACAGTTGTGTGATTGGTGGAGTGTTGTTATTCTTTTGAAATGT 306
q	3001	aggatacacacagttgtgtgattggtggagtgttggtgttattctttttgaaatgt 306
0 y	3061	PCTTGGCACAAACACCATTAGAAACACAAATGAAGGTTATCA
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y do	3121	STGGCARANTECTETCACATTCCACACAGAGCTRAACTTCAGAGCTTCTGATC 3180 
Qy	3181	THATTATAAACTTTGCCGAGGACCCGAAGATCGCTTAGGCAAGAATGGTGCTGATGAA 3240

"contains 10 copies of GGC repeat, similar to repeats that undergo expansion in human diseases associated with neuronal

/note= /\*tag= /\*tag=

phenotypes" 395.3787

/\*tag= c 3788..7382 /\*tag= d

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6058.

/\*tag= e /note= "Alu-J subfamily repeat motif"

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replace(978,G)

/\*tag=

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Flanagan P, Plowman
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P-PSDB; AAY06526.
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                                      CTICATACATICCIAAAAICACACACACAGAIACAICAAATITIGAICCIGIIGAIC 3360
                                                                             TATATATGTGTGCTCTGTGTACAATATTTTATTTCCTAAATTATGGGAAATCCTTTTAA
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/note= "deletion of 2 adenines, causes
frameshift"

99WO-US01145.

98US-0072023

/note= "silent polymorphism" replace(3252.3253)

/\*tag=

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This is the nucleotide sequence of a cDNA clone coding for a human orthologue, i.e. hWaRT1 (see AAV06526). of Drosophila non-receptor serine/threconine kinase WART. hWART1 cDNA was isolated from a human bone marrow, cDNA library using PCR fragments of hWART1 as probes. 3 Polymorphisms were identified in the hWART1 gene: (1) at nucleotide 978, resulting in an Ala/Guy change; (2) at nucleotide 1840, silent; and (3) at nucleotides 3252-3253, comprising a deletion of 2 adenosines, resulting in a C-terminal truncation of hWART1 in the putative kinase domain. The latter frameshift marrow cDNA. Truncation of hWART1 could play a role in disease consmall cell lung cancer, ovarian tumours, central nervous system tumors, renal tumours and breast tumours, and may provide a target to non-small cell lung cancer, ovarian tumours, entral nervous system tumors, renal tumours and breast tumours, and may provide a target coroclogy drug development. Nucleic acids encoding full-length wARRT1 and hWART1 polypeptides lacking one or more of amino acid segments 12-45, 55-151, 236-377, 404-520, 555-559, 601-702, 691-998, cand 1011-1086, or lacking one or more of the N-terminal domain, catalytic domain, or C-terminal domain are claimed, as well as the control of the N-terminal domain, catalytic domain, or C-terminal domain are claimed, as well as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibodies, a method for identifying modulators of hWART function, and use of such modulator compounds to treat an abnormal condition involving hWART signal transduction, especially cancer. Probes for detection of hWART nucleic acids are also claimed.
New nucleic acid encoding human orthologs of Drosophila WART proteins, used to identify specific modulators for treating or for diagnosis
                                                                                                                                                                                                                                       Claim 1; Page 120-121; 137pp; English
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human; signal transduction; diagnosis; therapy; ss.

WART1; hWART1; WART orthologue; protein kinase; cancer; tumour;

Homo sapiens

Key 5'UTR

AAX87396 standard; cDNA; 7382

RESULT 3

AAX87396;

(first entry)

Human WART1 cDNA. 08-OCT-1999

Location/Qualifiers 1..399

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The present sequence is useful for treating cancer that is refractory to standard chemotherapy or radiation therapy such as hyperplasia, on dysplasia, and disorders associated with aberrant levels of cdc2 activity. Conditions treated by promoting cdc2 function include degenerative disorders, proxth deficiencies, hypoproliferative disorders, physical trauma, lesions, and wounds: An animal model preferably a mouse, in which a lats gene has been disrupted by homologous recombination, e.g. a lats knock out mouse, is used for screening compounds that can be used to treat or prevent cancer, particularly skin cancer, soft tissue sarcomas and ovarian tumours, and disorders associated with pituitary dysfunction e.g. luteinizing hormone (LH) hypogonadotropic hypogonadism. The lats DNA is also used in gene therapy.
                                                                                                                                                                                                                                                                                                                                           Use of lats proteins, complexes of lats and cdc2 for treating cancer that is refractory to treatment by standard chemotherapy and radiation therapy, and disorders associated with aberrant levels of cdc2 activity
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CCACCACCTCCAAGAGGCCAGACTCCCCCTCCAAGAGGTACAACTCCACCTCCCCCTTCA 1031 180 911 851 971 791 9 Gaps 1 GTGCAACATTCAATTAACCGAAAACAAAGCTGGAAAGGTTCTAAAAGAGTCTCTAGTTCCT GTGCAGCAATCAGTTAACCGCAAACAGAGCTGGAAAGGTTCTAAAGAATCCTTAGTTCCT CAGAGGCATGGCCCGCCACTAGGAGAAAGTGTGGCCTATCATTCTGAGAGTCCCAACTCA CAGACAGATGTAGGAAGACCTTTGTCTGGATCTGGTATATCAGCATTTGTTCAAGCTCAC CCTAGCAACGGACAGAGAGTGAACCCCCCACCACCACCTCAAGTAAGGAGTGTTACTCCT DB 21; Length 3213; 62.3%; Score 2483; DB 21; Length larity 87.4%; Pred. No. 0; Conservative 0; Mismatches 385; Indels Best Local Similarity Matches 2769; Conserv Query Match 792 912 732 61 352 121 181 972 g qq a g ò ò ò

1211 1331 1511 1017 1811 1077 1871 2111 1151 1391 1451 1571 1631 1691 1751 GAAGCICCAAACTATCAAGGACCACCACCACCTACCCAAAACAICTGCTGCACCAAAAC 1931 CCATCTGTTCCTCCATACGAGTCAATCAGTAAGCCTAGCAAAGAGGATCAGCCAAGCTTG 1991 540 420 597 657 717 837 897 957 GCTTTACAAACAGGGGGATCTGCTGCTCCTTCGTCATATACAAATGGAAGTATTCCTCAG TGGGAACCAAACTCTCAAACAAAGCGCTATTCTGGAAACATGGAATACGTAATCTCCCGA CAACCAATCATCATGCAGAGTTCTAGCAAATTTAACTTTCCATCAGGGAGACCTGGAATG 1332 GTGAATCGGCAGCCACCACCTCCATATCCTCTGACAGCAGCTAATGGACAAAGCCCTTCT TCTATGATGGTGCCAAACAGAAATAGTCATAACATGGAACTATATAACATTAGTGTACCT GGACTGCAAACAAATTGGCCTCAGTCATCTTCTGCTCCAGCCCAGTCATCCCCGAGCAGT GCAATTACACCAGCTCCTATTCAACAGCCTGTGAAAAGTATGCGTGTATTAAAAACCAGAG CAACCCAGTCCTTTTCCTGAGGGAACCGCTTCAAATGTGACTGTGATGCCACCTGTTGCT CCCAAGGAAGATGAGAGTGAAAAGAGTTATGAAAATGTTGATAGTGGGGATAAAGAAAAG **AAACAGATTACAACTTCACCTATTACTGTTAGGAAAAACAAGAAGATGAAGAGGGGAAGG** ATCTCTCCTGTCCCACCTGGGGCATGGCAAGAGGGCTATCCTCCACCACCTCTCAACACT TCCCCCATGAATCCTCCTAATCAAGGACAGAGGCCATTAGTTCTGTTCCTGTTGGCAGA CAGAATGGTACTGGACAAACTGATTTCATGATACACCAAAATGTTGTCCCTGCTGGCACT GGGCATGAAATCCCTACATGCCAACCTAACATACCAGTGAGGTCAAATTCTTTTAATAAC CCATTAGGAAATAGAGCAAGTCACTCTGCTAATTCTCAGCCTTCTGCTACAACAGTCACT CTACAGACTGCTTTAGCACCTACACACCCTTCTTGGATACCACAGCCAATTCAAACTGTT 481 1272 1392 1452 1512 1018 1032 1092 1212 1572 1692 1078 1872 301 361 1152 421 1632 1752 1812 1138 1258 2052 928 1992 1932 ò g ò а ò g δ g ò g ò q

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                                                                                                                                                                                                               This sequence encodes a mouse large turmour suppressor m-lats protein, and has been isolated from a newborn mouse brain phage lambda 2AP cDNA library using a 2.2-kb DNA probe from the Drosophila lats gene (AAT42117). A homologous mouse sequence has also been isolated (m-lats2, AAT42120). The gene encodes a putative protein-serine. The gene encodes a putative protein-crucial role throughout development. Activators or inhibitors of lats function (e.g. an antisense oligonucleotide or dominant-negative
                                                                                                                                                                                                                                                                                                           lats fragment) may be used in therapy of cancer or other proliferative disorders, degenerative disorders, trauma, growth deficiency, etc., and fragments of the gene may be used as diagnostic probes. A lats inhibitor sequence may be expressed in a transgenic plant or farm animal to confer increased growth and inhibit
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Pred. No. 0;
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Best Local Similarity 87.3%;
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cell regulation; cell proliferation; cell differentiation; tumour;
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Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; ohemotraxis; chemokinesis; thrombolysis, oncogenesis; proliferation; metastiasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; atheroscierosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
                                        3390 GAAGAAAATGTAAATGACACTCTCAAT-GGATGGTATAAAAATGGAAAGCATCCTGAACA 3448
1021 CAAGCTAAACTCAGTCCTGAAGCTTCTGATCTTATTAAAACTTTGCCGAGGACCCGAA 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a medical condition in a mammalian subject
                                                                                                                                         ACAGATACATCAAATTTTGATCCTGTTGATCCTGATAAATTATGGAGTGATGATAACGAG
                           GATCGCTTAGGCAAGAATGGTGCTGATGAAATAAAAGCTCATCCATTTTTAAAACAATT
                                                                                TGCATTCTATGAATTTACCTTCCGAAGGTTTTTTGATGACAATGGCTACCCATA 3502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for preventing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell culture; drug screening; gene therapy; antlinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerot
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human large tumour suppressor 1 homologue cDNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antifungal; vulnerary; antiulcer; ss
                                                                                                                                                                                                                                                                                                                                                     ABA08740 standard; cDNA; 1357 BP
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                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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P-PSDB; ABB11496.
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polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may differentiation activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; has memorated activity; cell proliferation or cell immunomodulatory activity; activit, or inhibin related activities; chrombotic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis.

CC thrombolytic activities; polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders telinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., myeloid or lymphoid cell conditions, bone disorders (e.g., osteoporosis), and abnormal crepair or netlinopathy atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal crepair (or nucleic acids encoding them) may be used to promote wound the immunomodulatory activities may be used in the treatment of viral, and phymorial and dingal indettions in addition to immune disorders. nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the Polypeptides with growth factor activity may be used in cell cultures t promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells autoimmune disease or accidental damage. The polypeptides and nucleoti may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding that can be used to augment or replace cells damaged by novel human polypeptide of the invention.

## Sequence 1357 BP; 436 A; 254 C; 285 G; 382.T; 0 other;

9

2455 2276 AAAGATGCTTTGCCAAAAAGAATCTAATTACATCCGTCTTAAAAGGGCTAAAATGGACAA 2335 TCTTCGAAATCAAGTCGCTCATGTTAAGGCTGAGAGAGATATCCTGGCTGAAGCTGACAA 2515 2516 TGAATGGGTAGTTCGTCTATATTATTCATTCCAAGATAAGGACAATTTATACTTTGTAAT 2575 299 360 AAGTCTGGCACGATTCTACATAGCAGAACTTACCTGTGCAGTTGAAAGTGTTCATAAAAT 419 Gaps 59 2396 AAGAAAAGTAGATACTAAGGCTTTGTATGCAACAAAAAACTCTTCGAAAGAAGAIGTTCT **AAGTCTGGCACGATTCTACATAGCAGAACTTACCTGTGCAGTTGAAAGTGTTCATAAAAT** 240 TGAATGGGTAGTTCGTCTATATTATTCATTCCAAGATAAGGACAATTTATACTTTGTAAT DB 22; Length 1357; 14; 23; Indels Score 1233.2; DB 2 Pred. No. 1.1e-298; 0; Mismatches 23; 0 31.0%; Conservative Local Similarity Matches 1321; Query Match 2456 2576 2636 g ò g ò g QΥ qq ò g ò g ŏ g

479

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The

differentiation;

cell

cell proliferation;

regulation;

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TAAATTGACTGACTTTGGCCTCTGCACTGGCTTCAGATGGACACACGATTCTAAGTACTA
        CTCAAGCTGTGGATGTGGAGACAGACTGAAGCCATTAGAGCGGAGAGCTGCACGCCAGCA
                                 TATCAACTGGCAAACATCTTCACATTCCACCACAAGCTAAACTCAGTCCTGAAGCTTC
                                                                                                                                                                                                                CCAGCGATGTCTAGCACATTCTTTGGTTGGGACTCCCAATTATATTTGCACCTGAAGTGTT
                                                                                                                                    GCTACGAACAGGATACACACAGTTGTGATTGGTGGAGTGTTGGTGTTATTTTGA
                                                                                                                                                                      AATGTTGGTGGGACAACCTCCTTTCTTGGCACAAACACCATTAGAAACACAAATGAAGGT
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                                                                                                                                                                                                                                                 TGAAATAAAAGCTCATCTTTTTAAAA---CAATTGACTTCT-CCAGTGACCTGA---
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gene fragment encoding a partial peptide fragment.
                                                                                                                                                  warts protein; Drosophila; protein kinase; epithelial
                      BP
                 AAX32984 standard; DNA; 795
                                                                                  (first entry)
                                                                                  30-JUN-1999
                                                                                                                   Human warts
                                                                                                                                                  Human;
AAX32984
ID AAX
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The invention relates to a human warts protein, homologous to Drosophilia warts gene expression product. The warts expression product is a protein kinase involved in the regulation of proliferation and differentiation of epithelial cells and suppression of tumour formation. The gene, its expression product and antibodies are useful in the study of the mechanisms of tumour development. The present sequence represents a human warts gene fragment encoding a partial peptide fragment.
tumour; ss
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Pred. No. 2.4e-187;
0; Mismatches 4;
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                                                                                                                                                                                         Nishiyama Y,
                                                                                                                                                                                                                                                                                      Disclosure; Page 58-60; 68pp; Japanese
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                                                                                                                                                                                                                                                          vertebrates homologous
                                                                                                                                                             ELECTRIC IND
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                                                                                                                                 97JP-0258689
                                                                                                                                                                                        Nagamine Y,
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Matches 791; Conservative
                                                                                                                                                                                                                  1999-244389/20.
                                                                                                                                                             ) SUMITOMO
                                                                                                                                                                                                                                P-PSDB; AAY06893
                                                                                                                                                                                        Kishimoto T,
                      sapiens
                                               WO9915558-A1
                                                                                                                                24-SEP-1997;
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 GGCACTGTGÄATCGGCAGCCACCACCTCCATATCCTCTGACAGCTAATGGACAAAGC 1385
                                                                                                                          GTACCTGGACTGCAAACAAATTGGCCTCAGTCATCTTCTGCTCCAGCCCAGTCATCCCCG 1565
                                                               099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isolated (m-lats, AAT42119). The gene encodes a putative proteinserine/threonine-kinase, and inhibits cell proliferation and plays a crucial role throughout development. Activators or inhibitors of lats function (e.g. an antisense oligonuclectide or dominant-negative
                                                                                                                                                GTACCTGGACTGCAAACAAATTGGCGTCAGTCATCTTCTGCTCCAGCCCAGTCATCCCCG 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence encodes a mouse large tumour suppressor m-lats2 protein, and has been isolated from a newborn mouse brain phage lambda-2AP cDNA library using a 2.2-kb DNA probe from the Drosophila lats gene (AAT42117). A homologous mouse sequence has also been
                                         CCTTCTGCTTTACAAACAGGGGGATCTGCTGCTCCTTCGTCATATACAAATGGAAGTATT
                                                    CCTCAGTCTATGATGGTGCCAAACAGAAATAGTCATAACATGGAACTATAACATTAGT
                                                                                            develop prods
proliferation
                                                                                                                                                                                                                                                                                                                                      protein-serine/threonine-kinase; cell proliferation; antisense; dominant-negative; cancer; degenerative disorder; trauma; growth deficiency; therapy; antitumour; vulnerary; diagnostic;
                                                                                                                                                                                                                                                                                                                                                                      transgenic plant; transgenic animal; growth; senescence; ds
                                                                                                                                                                                                                                                                                                                             gene; large tumour suppressor; fetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lats function (e.g. an antisense oligonucleotide or domi
lats fragment) may be used in therapy of cancer or other
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enhancing p
                                                                                                                                                                                                                                                                                                       M-lats2 gene encoding large tumour suppressor
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proliferative disorders, degenerative disorders, trauma, growth deficiency, etc., and fragments of the gene may be used as diagnosti probes. A lats-inhibitor sequence may be expressed in a transgenic plant or farm animal to confer increased growth and inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1773 ACACACCCTTCTTGGATACCACAGCCAATTCAAACTGTTCAACCCAGTCCTTTTCCTGAG
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llarity ,63.78;
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                             2598 ATGATGAGCCTATTAATTAGAATGGGCATCTTTCCAGAAAGTCTGGCACGATTCTACATA
                                          GCAGAACTTACCTGTGCAGTTGAAAGTGTTCATAAAATGGGTTTTATTCATAGAGATATT
                                                                                                                                                    TGCACTGGGTTCAGATGGACACGATTCTAAGTACTATCAGAGTGGTGACCATCCACGG
                                                                                                             2838 CAAGATAGCATGGATTTCAGTAATGAATGGGGGGGATCCCTCAAGCTGTCGATGTGGAGAC
                                                                                                                                                                                                                                   AGACTGAAGCCATTAGAGCGGAGAGCTGCACGCCAGCACCAGCGATGTCTAGCACATTCT
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Soft tissue sarcoma; pituitary disorder; gene therapy; hyperplasia; LH; luteinizing hormone hypogonadotropic hypogonadism; metaplasia; dysplasia; degenerative disorder; growth deficiency; physical trauma; hypoproliferative disorder; lesion; wound; lats knock-out mouse; ds.
                                                                                             Mouse; Lats2; large tumour suppressor; cytostatic; vulnerary; cell overproliferation inhibitor; cdc2; cell cycle-dependent kinase; treatment; prevention; screening; cancer; skin; ovarian tumour;
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/note= "This region is missing in the mouse Lats2
DNA sequence shown in figure 14"
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/note= "This region is erroneously repeated i
mouse Lats2 DNA sequence shown in figure 14"
1921..2960
                                                    Mouse Lats2 (large tumour suppressor) DNA.
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                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                    (first entry)
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970..1920
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                                                                                                                                                                                                                                                      Mus musculus.
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                  21-JUN-2000
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Xu T, Tao W, St John MAR, Fei X, Fukumoto RK, Zhang S; Turenchalk GS, Stewart RA;

980s-0096996. 980s-0096997.

18-AUG-1998;

L8-AUG-1998;

(UYYA ) UNIV YALE.

WPI; 2000-246496/21. P-PSDB; AAY70392. Use of lats proteins, complexes of lats and cdc2 for treating cancer that is refractory to treatment by standard chemotherapy and radiation therapy, and disorders associated with aberrant levels of cdc2 activity

Claim 44; Pages 112-117; 134pp; English.

The present sequence is a DNA encoding mouse Lats2 (large tumour suppressor) protein which is a cell overproliferation inhibitor and a negative regulator of cell cycle-dependent kinase cdc2/cyclin A. The present sequence is useful for treating cancer that is refractory to standard chemotherapy or radiation therapy such as hyperplasia, to syplasia, and disorders associated with aberrant levels of cdc2 activity. Conditions treated by promoting cdc2 function include degenerative disorders, growth deficiencies, hypoproliferative preferably a mouse, in which a lats gene has been disrupted by homologous recombination, e.g. a lats knock-out mouse, is used for screening compounds that can be used to treat or prevent cancer, particularly skin cancer, soft tissue sarcomas and ovarian tumours, and disorders associated with pituitary dysfunction e.g. luteinizing hormone (LH) hypogonadotropic hypogonadism. The lats DNA is also used in gene therapy.

Sequence 3155 BP; 751 A; 924 C; 894 G; 586 T; 0 other;

BP.

AAZ51507 standard; DNA; 3155

RESULT 11

AA251507

AA251507

HXX

Owery Match
19.1%; Score 760; DB 21; Length 3155;
Best Local Similarity 63.7%; Pred. No. 6.8e-180;
Matches 1197; Conservative 0; Mismatches 665; Indels 18;

Gaps

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3 CACTCTGCTAATTCTCAGCCTTCTGCTACAACAGTCACTGCAATTACACCAGCTCCTATT	3 CAACAGCCTGTGAAAAGTATGGGTGTATTAAAACCAGAGCTACAGACTGCTTTAGCACCT	3 ACACACCCTTCTTGGATACCACAGCCAATTCAAACTGTTCAACCCAGTCCTTTTCCTGAG		3 CCACCACCACCTACCCAAAACATCTGCTGCACCAAAACCCCATCTGTTCCTCCTCATACGAG	3 TCAATCAGTÂAGCCȚAGCAAGAGCATCAGCCAAGCTTGCCCAAGGAAGATGAGAGAAA SACTGCCCAAGGAAGATGAGAGAGAGAGAGAGAGAGAGAGA	3 AAGAGTTA	ATTACAACTICCACCTATTACTGTTAGGAAAAACAAGAAGAATGAAGGGGAGGGGAATCT	CGTATTCAAAGTTATTCTCCTCAAGCATTTAAATTCTTTATGGAGCAACATGTAGAAAAT	3 GTACTCAAATCTCATCAGCAGCGTCTACATCGTAAAAAACAATTAGAGAATGAAATGATG 	B CGGGTFGGATTATCTCAAGATGCCCAGGATCAAATGAGAAAGATGCTTTGCCAAAAAGAA   1   1   1   1   1   1   1   1   1	3 TCTAATTACATCCGTCTTAAAAGGGCTAAAATGGACAAGTCTATGTGAGAGATAAG 	acactaggaataggagcatttggtgaagtctgtctagcaagaaagtagatactaaggct 	3 TTGTATGCAACAAAAACTCTTCGAAAGAAAGGTGTTCTTCTTCGAAATCAGTCGCTCAT	GTTAAGGCTGAGAGAGATATCCTGGCTGAAGCTGACAATGAATG	3 TATTCATTCCAAGATAAGGACAATTTATACTTTGTAATGGACTACATTCCTGGGGGTGAT	ATGATGAGCTATTAATTAGAATGGCCATCTTTCCAGAAAGTCTGGCACGATTCTAGATA	3 GCAGAACTTACCTGTGCAGTTGAAAGTGTTCATAAAATGGGTTTTATTCATAGAGATATT 
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2244 2605 TICAACACCATCGACTTTTCCCGTGACATCCGAAAGCAGGCTGCACCCTACGTCCCCACC 2664 2897 2957 2364 2424 2425 TTCTTGGCCCCCACCCCCACGCAGCAGAGGTGAAGGTGATCAACTGGGAGCACGCTG 2484 CGAGGACCCGAAGATCGCTTAGGCAAGAATGGTGCTGATGAAATAAAAGCTCATCCATT 3257 TTTAAAACAATTGACTTCTCCAGTGACCTGAGACAGCAGTCTGCTTCATACATTCCTAAA 3317 ATCACACACCCAACAGATACATCTTTGATCCTGTTGATCCTGATAAATTATGGAGT 3377 2665 ATCAGCCACCCCATGGACACCTCCAATTTTGACCCGGTGGATGAAGAAAGCCCCTGGCAC 2724 2781 2125/TGCACTGGATTCAGGTGGACTCACAATTCCAAGTACCAGAAAGGGAACCACACATGAGA 2184 TIGIGIGATIGGIGGAGIGITGGIGTTATICTTTTGAAATGTIGGIGGGACAACCTCCT 3077 3078 TICTIGGCACAAACACCATIAGAAACACAAAIGAAGGTTATCAACTGGCAAACAICTCTI 3137 2958 TTGGTTGGGACTCCCAATTATTGCACCTGAAGTGTTGCTACGAACAGGATACACACA 3017 CACATTCCACCACAAGCTAAACTCAGTCCTGAAGCTTCTGATCTTATTAAAACTTTGC 3197 AGACTGAAGCCATTAGAGCGGGAĠAGCTGCACGCCAGCACCAGCGATGTCTAGCACATTCT 1365 CTCTGTGACTGGTGGAGGCGTCGGTGGTTCTTTTGAGATGCTGGTTGGCAGCGCCT TGCACTGGCTTCAGATGGACACACGATTCTAAGTACTATCAGAGTGGTGACCATCCACGG 2838 CAAGATAGCATGGATTTCAGTAATGAATGGGGGGATCCCTCAAGCTGTCGATGTGGAGAC WART2; hWART2; WART orthologue; human; sign protein kinase; cancer; tumour; diagnosis; AAX87397 standard; cDNA; 5276 BP 2842 CCCTTCCGGTGCCCGAAGCC '2861 CCATATAATTATCCGAAGCC 3517 08-OCT-1999 (first entry) Human WART2 cDNA. Homo sapiens AAX87397; 3018 2778 2898 3138 3198 3258 3318 3378 3498 RESULT 12 AAX87397 g qq Op δ qq ò Db δ ద δ q ŏ g δ ò δ g δ qq ò a Ω q g ò 

Location/Qualifiers

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Y A	(SUGE-) SUGEN	SUGEN INC.	,						
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XEEE;	New nucleic acid proteins, used to or for diagnosis	New nucleic acid encoding human orthologs of Drosophila WART proteins, used to identify specific modulators for treating or for diagnosis	orthologs o ific modulat	of Drosophil ors for tre	ohila WART treating cancer		ä . ·		
PS	Claim 1; Page	Claim 1; Page 122-123; 137pp; English	nglish.				* *		
SS	This is the n		of a cDNA c	lone coding	for a human				
ខ្លួ	orthologue, i.e. hWART2 serine/threonine kinase		AY06527), of Drosophila non-rec hWART2 cDNA was isolated from	Drosophila was isolate	(see AAY06527), of Drosophila non-receptor WART: hWART2 cDNA was isolated from a			:	
ပ္ပင္ပ	human bone marrow	human bone marrow cDNA library using	using a PCR	fragment of hWART1	hWART1 as	. ,			
ខ្ល	lines, except	consist Ost of	entry expressed in numa the colon cancer lines	ines examined.	our cells	٠.			
ပ္ပင္ပ	overexpression in tumour		<u>.</u>	l tissues m	ä.				
ខ្លួ	target ror oncology full-length hWART2	for oncology drug development.	oment. Nucl	eic acio lacking	ls encoding		'		
8	amino acid se	amino acid segments 1-33, 43-139, 342-466,	9, 342-466,	467-480, 51		\$* *		-	
ပ္ပင္ပ	and 974-1048, or	and 974-1048, or lacking one or more of the N-terminal domain,	more of the	N:terminal	domain,		. •		
ខ	hWART1 sequen		ART2 and hwa	RT1 polypep	tides,		•		
ပ္ပင္ပ	antibodies, a	a method for identifying modulators	fying modula	tors of hWART	RT function,				
ខ	involving hWART	such modulator compounds to treat an abnormal WART signal transduction especially cancer	inds to treat an	ally cancer	al condition Probes for				
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S	Sequence 5276	5276 BP; 1348 A; 1407 C; 1345	ë	1176 T; 0 ot	other;			_	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human growth hormone inhibited tumour suppressor genes 1 and 2 diagnosis of dwarfism, gigantism, acromegaly, angiopathy, diabetic
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tumours including breast cancer, renal adenocarcinoma, colorectal cancer, and leukaemia. Antibodies against the proteins can be used is diagnostic pharmaceutical preparation for examining expression of
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                                                                                                          5486 BP; 1378 A; 1452 C; 1390 G; 1266 T; 0 other;
                                                                                                                                                Score 744.4; DB 21; Length
Pred. No. 7.2e-176;
0; Mismatches 556; Indels
                                                                                                                                                  18.7%;
                                                                                                                                                                       Best Local Similarity 66.3
Matches 1123; Conservative
                                                                 a tumour suppressor gene.
                                                                                                            Sequence
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                                                                                                                                                                                                                             Human: growth hormone inhibited tumour suppressor protein; he antinoplastic; dwarfism; gigantism; acromegaly; angiopathy; diabetic nephropathy; cardiopathy; tumour; breast cancer; renal adenocarcinoma; colorectal cancer; leukaemia; ss.
                                                                                                                                                                                         DNA encoding a tumour suppressor protein hGHITS2.
                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                          BP.
                                                                          DNA; 5486
                                                                                                                                                      (first entry)
                                                                        AAA59130 standard;
                                                                                                                                                  07-NOV-2000
                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                             AAA59130;
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2280 ATGCTTTGCCAAAAAGAATCTAATTACATCCGTCTTAAAAGGGGCTAAAATGGACAAGTCT

Key

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes a human growth hormone inhibited tumour suppressor (hGHITS) protein. The hGHITS proteins can be used in an antineoplastic pharmaceutical preparation. Probes for the hGHITS DNA sequences can be used in diagnostic pharmaceutical preparations. The diagnostic pharmaceutical preparations can be used for examining expression of hGHITS genes in dwarfism, giantism, acromegaly, angiopathy, diabetic nephropathy or cardiopathy; or in malignant tumours including breast cancer, renal adenocarcinoma, colorectal cancer, and leukaemia. Antibodies against the proteins can be used in a tumour suppressor gene.
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                                               "tumour suppressor protein"
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Pred. No. 7.2e-176;
0; Mismatches 556;
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66.3%;
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387..3653
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Matches 1123; Conservative
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                      2760 TTGACTGACTTTGGCCTCTGCACTGGCTTCAGATGGACACACGATTCTAAGTACTATCAG
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ATCCTCTACCAGAAAGAGTCTAATTACAACAGGTTAAAAGAGGGCCAAGATGGACAAGTCT
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                                                                      TACATTCCTGGGGGTGATATGATGAGCCTATTAAATTAGAATGGGCATCTTTCCAGAAAGT
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The present sequence encodes a partial polypeptide which has kinase activity. The kinase polynucleotides can be used to express the polypeptides, and as probes to identify nucleic acids encoding proteins having kinase activity. The kinase polypeptides and fragmented polypeptides are used as molecular weight and isoelectric focusing markers, and as controls for peptide fragmentation. They also have a number of therapeutic uses as kinases play a central role in cellular signal transduction. The polypeptides could also be used to identify binding partner proteins. The polypeptides can also be used a reagent to identify any proteins that the polypeptide regulates, and proteins with which it might interact. The polypeptides may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preparation of antibodies. The antibodies can be used in detect the presence of the protein, and to purify the protein
3420 TGGTATAAAAATGGAAAGCATCCTGAACATGCATTCTATGAATTTACCTTCCGAAGGTTT 3479
                                                                        marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human kinase polypeptides and polynucleotides used as molecular weight markers and as controls for peptide fragmentation
                ACCTGCCCAATAACAAGCATCCTGAGCACGCATTTTACGAATTCACCTTCCGAAGGTTC
                                                      TTTGATGACAATGGCTACCCATATAATTATCCGAAGCCTATTGAATATGAATACATTAAT
                                                                                                                                                                                                                                                                                                                             activity; molecular weight marker; isoelectric focusing m
fragmentation control; cellular signal transduction; ss.
                                                                                                                                                                                                                                                                                               cDNA SS1771A encoding a partial protein kinase.
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/note= "partial sequence"
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DB 21; Length 1961;

504 A; 550 C; 539 G; 368 T; 0 other;

Sequence 1961 BP;

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Query Match

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2al Similarity 66.2%; Pred. No. 1.1e-175;	GAAGGCCCAGAGCGGGGGCCTCCCCTACCGAAACATCTGCTGCACC	27 AAAA CCCATCTGTCCTCCATACGAGTCAATCAGTAAGCCTAGCAAAGAGGATCAG	ъ н	040 GATAAAGAAAAGAACAGATTACAACTTCACCTATTACTGTTAGGAAAAACAAGAAAGA	100 GAAGAGCGAAGGGAATCTCGTATTCAAAGTTATTCTCCTCAAGCATTTAAATTCTTATG 	160 GAGCAACATGTAGAAAATGTACTCAAAATCTCATCAGCAGCGTCTACATCGTAAAAAAAA	220 TTAGAGAAAGGAAATGGGGGTTGGATTATCTCAAGATGCCCAGGATCAAATGAGAAAG 	280 ATGCTTTGCCAAAAGAATCTAATTACATCCGTCTTAAAAGGGCTAAAATGGACAAGTCT 	340 ATGTTTGTGAAGATAAAGACACTAGGAATAGGAGCATTTGGTGAAGTCTGTCT	400 AAAGTAGATACTAAGGCTTTGTATGCAACAAAAACTCTTCGAAAGAAA	460 CGAAATCAAGTCGCTCATGTTAAGGCTGAGAGATATCCTGGCTGAAGCTGAGAATGAA 	20 TGGGTAGTTCGTCTATATTCATTCCAAGATAAGGACAATTTATACTTTGTAATGGAC.	30 TACAȚTCCTGGGGGGGGTGATATGAGCCTATTAATTAGAATGGCCATCTTTCCAGAAGT 	10 CTGGCACGATTCTACATAGCAGAACTTACCTGTGCAGTTGAAAGTGTTCATAAAATGGGT 	00 TITATICATAGAGATATTAAACCIGATAATATITIGATIGATIGGIGGICATAATAAA 	60 TIGACTGACTTTGGCCTCTGCACTGGCTTCAGATGGACACACGATTCTAAGTACTATCAG 	80 AGTGGTGACCATGGCAAGATAGCATGGATTTCAGTAATGAATG	00 AGCTGTCGATGTGGAGACAGAGCCATTAGAGCGGAGAGCTGCACGCCAGCAGGAGTTGTTGTTTAGAGCGAGAGAGTGCAGCAGCAGCAGCAGGAGTTAGAGAGAG
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1161 CGCAAAGGGTACACTCAACTCTGTGACTGGTGGTGTTGGAGTGTTCTTTCGAGATG 1220
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2940 CGATGTCTAGCACATTCTTTGGTTGGGACTCCCAATTATATTGCACCTGAAGTGTTGCTA 2999
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Search completed: January 16, 2003, 10:32:01 Job time: 562.163 secs Appli Appli Appli Appli Appli

Sequence Sequence Sequence

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APPLICANT: Xu, Tian
APPLICANT: Tao, Wufan
APPLICANT: Wang, Weiyi
APPLICANT: Zhang, Sheng
APPLICANT: Yu, Wan
TITLE OF INVENTION: GENES AND METHODS BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: ISOPPY disk
COMPUTER: ISOP Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DAFA:
APPLICATION NUMBER: US/09/442,100
                                 US-09-225-749-24
US-09-289-466-2
US-09-289-466-1
US-09-289-466-1
US-09-430-564-1
US-08-422-699A-8
US-08-422-699A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6523-003
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/411,111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (212) 790-9090
(212) 869-9741/8864
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TELEFAX: (212) 869-9741/8
TELES: 66141 PENNIE
TELES: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
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STRANDEDNESS: double
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CORRESPONDENCE ADDRESS:
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LOCATION: 231..3623
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                           441362 seqs, 153338381 residues
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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                                                              Patentin Release #1.0; Version #1.30
                                                                                      APPLICATION NUMBER: US/09/442,100
                                                 PC-DOS/MS-DOS
                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/411,111
                                                                                                                                                                                                                             TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-971/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                               NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18, 972
REFERENCE/DOCKET NUMBER: 65,
TELECOMMUNICATION:
                                     IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 62.3%;
Best Local Similarity 87.4%;
Matches 2769; Conservative
                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                              ENGTH: 3213 base pairs
                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
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                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA
                                                   OPERATING SYSTEM:
10036-2711
                                                                                                                  CLASSIFICATION:
                                                                                                                                                        FILING DATE:
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US-09-442-100-5
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	2352 ATAAAGACACTAGGAATAGGAGCATTTGGTGAAGTCTGTCT	2412 AAGGČTTGTAGGAACAAAAACTCTTCGAAAGAAAGATGTTCTTCGAAATCAAGTC 11	72 GCTCATGTTAAGGCTGAGAGATATCCTGGCTGAAGCTGACAATGAATG	JATIGTGAAAGGGGAGGAGGGATATCCTAGCAGAAGCCGACAATGAGTGGGGGGGTGGTC TATTAȚTCATTCCAAGATAAGGACAATTTATACTTTGTAATGGACTACATTCCT		2592 GGTGATATĠATGAGCCTATTAATTAGAATGGCCATCTTTCCAGAAAGTCTGGCACGATTCT	2652 TACATAGCAGAACTTACCTGTGCAGAGGTTCAAAGGGTTTTATTCATAGA	۰ ،	1978 GATATTAAACCIGATAACATTIGATIGATIGATIGATIGATIGATITAAATTAAAT	2772 GGCCTCTGCACTGCCTTCAGATGGACACACGATTCTAAGTACTATCAGAGTGGTGACCAT 111   11111111111111111111111111111111	י פ	2032 CONCOCANGETAGE ATTITUDATE TO ASTAURA AS SOCIO AND ASTAURANT TO ASTAURANT AS AS	cn .	2158 GGGGACAGACTGAAGCCACTGGAGCGGAGAGCTGCTCGCCAGCACCAGCGATGTCTAGCC	2952 CATTCTTTGGTTGGGACTCCCAATTATATTGCACCTGAAGTGTTGCTACGAACAGGATAC	3012 ACACACTTGTGTGATTGGTGGAGTGTTGTTGTTTTTTGAAATGTTGGTGG	2278 ACACAGCTGTGTGACTGGTGGAGTGTTGGTGATTTTTTTT	3072 CCTCCTTTCTTGGCACAAACACCATTAGAAACACAAATGAAGGTTATCAACTGGCAAAACAAAC	32 T	2398 TCTCTACACATCCCTCCTCAAGCTAAGCTGAGCTCGAAGCTCTGACCTCATTATCAAA	O 10	38 CIGIGICGAGGACCAGAAGACCGCCICGGCAAGAACGGIGCIGGIGAGAIAAAGG	3252 CCATTTTTTAAAACAATTGACTTCTCCAGTGACCTGAGACAGCAGTCTGCTTCATACATT [	3312 CCTAAAATCACACACCCAACAGATACATCATTGATCCTGTTGATCCTGTAAATTA	3372 TGGAGTGATGATAACGAGGAAGAAATGTAAATGACACTCTCAATGGATGG	
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                                                                 3492 GGCTACCCATATAATTATCCGAAGCCTATTGAATATGAATACATTAATTCACAAGGCTCA 3551
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Sequence 7, Application US/09442100
Patent No. 6359193
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APPLICATION NUMBER: 08/411,111
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66141 PENNIE
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REGISTRATION NUMBER: 18,972
REFERENCE/DOCKET NUMBER: 657
TELECOMMUNICATION INFORMATION:
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APPLICANT: Yu, Wan
TITLE OF INVENTION: NUCLEY
TITLE OF INVENTION: GENES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADBRESS:
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Tao, Wufan
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ZIP: 10036-2711
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CITY: Ne
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                                                                                                                                                          Length 3155;
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                                                                                                                                                          Score 760; DB 4;
Pred. No. 5.2e-188;
                                                                                                                                                                                     0; Mismatches 665;
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63.7%;
INFORMATION:FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3155 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
                                                                                                                                                                                      Conservative
                                                                              MOLECULE TYPE: CDNA
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                                                                                                         : NAME/KEY:
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US-09-442-100-7
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1638 TTTGATGACAATGGCTACCCTTTCGATGCCCAAAGCCTTCAGGAGCATCACAG 1697
AGCTGTCGATGTGGAGACAGACTGAAGCCATTAGAGCGGAGAGCTGCACGCCAGCACCAĞ
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US-09-509-902A-6
Sequence 6, Application US/09509902A; Patent No. 6387676
GENERAL INFORMATION:
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Pred. No. 1.2e-183;
0; Mismatches 557;
                                            APPLICANT: Virca, Duke
APPLICANT: Bird, Timothy A.
APPLICANT: Marderson, Dirk M.
APPLICANT: Marken, John S.
TITLE OF INVENTION: Human cDNAS Encoding Pol
FILE REFERENCE: 2877-US
CURRENT APPLICATION UNBER: US/09/509,902A
CURRENT FILING DATE: 1999-08-03
NUMBER OF SEO ID NOS: 16
         Sequence 15, Application US/09509902A Patent No. 6387676 GENERAL INFORMATION:
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Best Local Similarity 66.2%;
Matches 1122; Conservative
                                                                                                                                                                 Patentin Ver. 2.0
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                                                                                                                                                                                                                 , ORGANISM: HOMO
US-09-509-902A-15
                                                                                                                                                                           SEQ ID NO 15
                                                                                                                                                                                                     TYPE: DNA
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27,60 TTGACTGACTTTGGCCTCTGCACTGGCTTCAGATGGACACCACGATTCTAAGTACTATCAG
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CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998 06-10
NUMBER OF SEQ ID NOS: 850-
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Patent No. 6262333
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APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Catino, Theodore J.
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Monahan, John E.
Schlegel, Robert
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Ford, Donna M.
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                                                       APPLICANT: Marken, John S.
TITLE OF INVENTION: Human cDNAs Encoding Polypeptides Having Kinase Functions
FILE REFERENCE: 2877-US
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pred. No. 3e-166;
); Mismatches 472; Indels 12;
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                                                                                     FILE REFERENCE: 2877-US
CURRENT APPLICATION NUMBER: US/09/509,902A
CURRENT FILING DATE: 1999-08-03
NUMBER OF SEQ ID NOS: 16
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67.2%;
                                       Anderson, Dirk M.
                                                                                                                                                                     PatentIn Ver. 2.0
     APPLICANT: , Virca, Duke
APPLICANT: , Bird, Timothy A.
                                                                                                                                                                                                                                                                                                                                      Conservative
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SEQ ID NO 6
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                                                                                                Length 638
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                                                                                               DB 4;
                                                                                                             .1e-149
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0; Mismatches
                                                                                             Score 609.8;
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 26 LENGTH: 638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09442100 Patent No. 6359193 GENERAL INFORMATION:
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                                                                                               15.3%;
98.4%;
                                                                                                          Similarity 98.4
27; Conservative
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APPLICANT: Yu, Wan
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Tao, Wufan
Wang, Welyi
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                                      TYPE: DNA
ORGANISM: Homo sapiens
US-09-328-111-26
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                             Query Match Best Local Simi
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APPLICANT:
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                                                                                                   SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                       PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/411,111
                                                                                                                                                                                                                                                                                                                                                                                         (212) 790-9090
(212) 869-9741/8864
                                                                             IBM PC compatible
                                                                                                                                                                                                                                                                                                                                 18,872
                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 69
TELECOMMUNICATION INFORMATION
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63.0%;
                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                          NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,8
                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5720 base pairs
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Matches 819; Conservative
                                                                                                                                        CURRENT APPLICATION DATA
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EDNESS: double
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                                                                                                                                                             APPLICATION NUMBER:
                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
               10036-2711
                                                                                                                                                                                                    CLASSIFICATION:
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USA
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                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                               COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY:
; LOCATION:
US-09-442-100-1
                                                                                                                    SOFTWARE:
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Length 678; Indels

Score 452.8; DB 4; Pred, No. 2.4e-108; 0; Mismatches 50;

11.4%;

548; Conservative

Similarity

= A,T,C or G

NAME/KEY: misc\_feature

FEATURE

CENGIH: 678

PRODUCTS

OF INVENTION: PROI REFERENCE: CCD-257

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CURRENT PEDLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 66
                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                           LOCATION: (1)...(678)
CTHER INFORMATION: n
US-09-328-111-66
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                                                                                                                             TYPE: DNA
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                                                                                                                                                                                       TCTAAGTACTATC---AGAGTGGTGACCATCCACGGCAAGATAGCATGGATTTCAGTAAT 2861
                                                                                                                                                 ACAÇAAATGAAGGTTATCAACTGGCAAACATCTCTTCACATTCCACCACAAGGTAAACTC
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                           ATCTITCCAGAAAGTCTGGCACGATTCTACATAGCAGAACTTACCTGTGCAGTTGAAAGT
                                        GATGGICATATTAAATTGACTGACTTTGGCCTCTGCACTGGCTTCAGATGGACACGAT
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                                                                                 2300 TAATTACATCCGTCTTAAAAGGGCTAAAATGGACAAGTCTATGTTTGTGAAGATAAAGAC 2359
                                                                                            2)14 IATTAAACCTGATAATATTTGATTGATC --GTGATGGTCATATTAAATTGACTGACTTT
                                                                                                                                                                                                                                                                                                                                               GATGAGCCTATTAATTAGAATGGGCATC-TTTCCAGAAAGTCTGGCACGATTCTACAT--
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                                                                                                                                                                                                                                                   2540 TICATICCAAGATAAGGACAATITATACTITGIAATGGACTACATTCCTGGGGGTGATAT
                                                                                                                                      GTATGCAACAAAAACTCTTCGAAAGAAAGAAGATGTTCTTCTTCGAAATCAAGTCGCTCATGT
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Sequence 11, Application US/08878989
Sequence 11, Application US/08878989
Patent No. 5885803
GBNERAL INFORMATION:
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TITLE

Lewis, Marcia E. Monahan, John E. Schlegel, Robert Ford, Donna M.

Burgess, Christopher C.
Bushnell, Steven E.
Carroll III, Eddie
Catino, Theodore J.
Derti, Adnan

APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT:

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986 ATGTATGAAATGCTAATAGGATATCCACCTTTCTGCTCTGAAACACCTCAAGAAACATAC 1045
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                                                                                                                                                                                                                                                               CATAAAATGGGTTTTAITCATAGAGATATTAAACCTGATAATATTTTGATTGATCGTGAT 2747
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   422 GATATGCTTGAAAAAGAGCAGGTGGCCCATATCCGAGCAGAAAGAGATATTTGGTAGAA 481
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                                                                          482 GCAGATGGTGCCTGGGTGGTGAGATGTTTTACAGTTTTTCAGGATAAGAGGAATCTTTAT
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Patent No. 6207148
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jenniff
APPLICANT: COTLEY, Nail C.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 AGGCAGAAGAAATTAGAAGTGGCCATGGAAGAAGAAGGATTAGCAGATGAAGAAAAAG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 TTACGTCGATCACAACACGCTCGCAAAGAACAGAGTTCTTACGGCTCAAAAGGACCAGA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2268 CAAATGAGAAAGATGCTTTGCCAAAAAGAATCTAATTACATCCGTCTTAAAAGGGCTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 2.3e-60;
0; Mismatches 516;
                                                                                                           ITILE OF INVENTION: DISEASE ASSOCIATED PROTEIN ITILE OF INVENTION: KINASES
                                                                                                                                                                                                                                                                                                                                                                        for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 269.4;
Pred. No. 2.
                                                                                                                                                                                      Incyte Pharmaceuticals,
                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF-0321
Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                        LACET: 3174 Porter Drive CITY: Palo Alto
                 Corley, Neil C.
Guegler, Karl G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.8%;
ilarity 53.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                  IBM Compatible
                                                     Lal, Preeti
Goli, Surya K.
Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1935 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Billings, Lucy J
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                  Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                            ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
                                                                                                                                                                                                                                                                                                                                                                    FastSEQ
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CLONE: 705365
                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 648; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
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                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                           COUNTRY:
                                    PPLICÁNT
                                                       PPLICANT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3108 ATGAAGGTTATCAACTGGCAAACATCTCTTCACATTCCACCACAAGCTAAACTCAGTCCT 3167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1046 AGAAAAGTGATGAACTGGAAAGAAACTCTGGTATTTCCTCCAGAGGTACCTATATCTGAG 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1223 AGGGAAAGGCCAGCAGCAATCCCTATAGAAATCAAAAGCATTGATGATACTTCAAATTTT 1282
482 GCAGATGGTGCCTGGGTGGTGAAGATGTTTTACAGTTTTCAGGATAAGAGGAATCTTTAT 541
                                                                                                                                                                                                                                                                                                     662 CACCAGTTGGGTTTCATCCATCGGGATATTAAGCCAGACAACCTTTATTGGATGCCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3168 GAAGCTTCTGATCTTATTATAAACTTTGCCGAGGACCCGAAGATCGCTTAGGCAAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1106 AAAGCCAAGGACTTAATTCTCAGATTTTGTATTGATTCTGAAAACAGAATTGGAAATAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3228 GGTGCTGATGAAATAAAAGCTCATCCATTTTTTAAAACAATTGACTTCTCCAGTGACCTG
                                                       2628 TTTCCAGAAAGTCTGGCACGATTCTACATAGCAGAACTTACCTGTGCAGTTGAAAGTGTT
                                                                                                                                                                                                                                                                       2748 GGTCATATTAAATTGACTGACTTTGGCCTCTGCACTGGCTTCAGATGGACACGATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2808 AAGTACTATCAGAGTGGTGACCATCCACGGCAAGATAGCATGGATTTCAGTAATGĀATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2928 GGCCAGCACCAGCGATGTCTAGCACATTCTTTGGTTGGGACTCCCAATTATATTGCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2988 GAAGTGTTGCTACGAACAGGATACACACAGGTTGTGTGATTGGTGGAGTGTTGGTGTTATT
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                                                                                                                                                                                                               602 TTGACAGAAGAGAAACACAGTTCTACATTTCAGAGACTGTTCTGGCAATAGATGCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Millward; Thomas A.
IITLE OF INVENTION: Nuclear DBF2-Related (NDR) Kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/08/860,150B CURRENT FILING DATE: 1997-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: PCT/EP95/05052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 94810746.1
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Patent No. 5981205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 4-20265/A/PCT
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EARLIER APPLICATION N
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APPLICANT: Millward;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           782 GAATTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        879 GACAA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 3348 GAT 3350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTGACAATGAATGGGTAGTTCGTCTATATTATTCATTCCAAGATAAGGAÇAATTTATAC 2567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 AGGCAGAAGAAATTAGAAGTGGCCATGGAAGAAGAAGGATTAGCAGATGAAGAGAAAAAG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 CTTGGCTTGGATGACTTTGAGTCTCTGAAAGTTATAGGAAGAGGAGCTTTTGGAGAGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 CGGTTGGTCCACAAAAAAAAATACAGGCCATATCTATGCAATGAAGATATTGAGAAAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 CAAATGAGAAAGATGCTTTGCCAAAAAGAATCTAATTACATCCGTCTTAAAAGGGCTTAAA
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                                                          ASSOCIATED PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 269.4;
Pred. No. 2.3
                                                                                                                                                                   Incyte Pharmaceuticals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/09/272,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Billings, Lucy J J
REGISTATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
FELECOMMUNICATION INFORMATION:
APPLICANT: GOli, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                    STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.8%;
ilarity 53.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                IBM Compatible
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LENGTH:, 1935 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION
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STRANDEDNESS: single
                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYNORAT04
                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
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Matches 648; Conserv
                                                                                                                                                                                                                     Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: line
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CLONE: 705365
US-09-272-796-11
                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                              CA
                                                                                                                                                                                                                                                                                                     94304
                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                2148 AAATTCTTTATGGAGCAACATGTAGAAAATGTACTCAAAATCTCATCAGCAGCGTCTACAT 2207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTGACAATGAATGGGTAGTTCGTCTATATTATTCATTCCAAGATAAGGACAATTTATAC 2567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1025 GCAGACAGTTTGTGGGTTGTGAAAATGTTCTATAGTTTTCAGGATAAGCTAAACCTCTAC 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITCINATGGACTACATICCTGGGGGTGATATGATGAGCCTATTAATTAGAATGGGCATC 2627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1205 CACCAACTIGGATTCATCACAGAGACATCAAACCAGACAACCTTCTTTGGACAGCAAG 1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTCATATTAAATTGACTGACTTTGGCCTCTGCACTGGCTTCAGATGGACACACGATTCT 2807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAATTTTATAGGAATCTGAACCACACCTCC-----CCAGTGATTTCACTTTCCAGAAC 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---GAAAGCAGAAACCTGGA 1409
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0; Mismatches 519;
EARLIER FILING DATE: 1994-12-22
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 53.6%;
Matches 645; Conservative
                                               Patentin Ver. 2.0
                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: (596)..(1990)
US-08-860-150-6
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                                                                                                             TYPE: DNA
ORGANISM: HOMO
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IITLE OF INVENTION: Nuclear DBF2-Related (NDR) Kinases
FILE REFERENCE: 4-20265/A/PCT
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Pred. No. 2e-
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CURRENT FILING DATE: 1999-06-22
EARLIER APPLICATION NUMBER: 08/860,150
EARLIER FILING DATE: 1997-06-19
EARLIER FILING DATE: 1997-12-20
EARLIER APPLICATION NUMBER: PCT/EP95/05052
EARLIER APPLICATION NUMBER: 94810746.1
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Patent No. 6040164
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Best Local Similarity 53.6%;
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US-09-338-132-6
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APPLICANT: Hemmings,
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 2160;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                           APPLICANT: Dietrich, Fred APPLICANT: Dietrich, Fred APPLICANT: Philippsen, Peter TITLE OF INVENTION: Fungal Target Genes and Methods FILE REFERENCE: PB/5-30908A CURRENT APPLICATION NUMBER: US/09/588,256 CURRENT FILING DATE: 2000-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGCTTCAGATGGACACACGATTCTAAGTACTATCAGA 2820
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                                                                                                                                                                                                                                                                                                                                                                                                                             No. 2.7e-35
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56.2%; Pred. No. 2.7¢
                                                                               Gates, Krista
Wendland, Juergen
Ayad-Durieux, Yasmina
                                                                                                                                                                                                                                               PatentIn Ver. 2.0
                                                                 Flavier, Albert
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 4.3'
Best Local Similarity 56.2'
Matches 325; Conservative
                                                Gaffney, Thomas
                                                                                                                                                                                                                                                                                                                ORGANISM: Ashbya gossypii
                                                                                                                                                                                                                                                                                                                                                           , LOCATION: (1)..(2160)
US-09-588-256-1
                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
Sequence 1, Applicat.
Patent No. 6291665
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
                                                                                                                                                                                                                                                                                 2160
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APPLICANT:
                                                APPLICANT:
                                                                                                                                                                                                                                                                  SEQ ID NO 1
                                                                                                                                                                                                                                                                                                  TYPE: DNA
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RESULT 14 US-08-860-150-1

AGGGTTCCACAAACGCATGACTCCAACTACTACAAGA 1405

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RESULT 13

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                                                                                                                                                                                                                                                                           3034 GIGTTGGTGTTATTCTTTTTGAAATGTTGGTGGGACAACCTCCTTTCTTGGCACAACAC
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Pred. No. 4.
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EARLIER FILING DAFE: 1995-12-20
EARLIER APPLICATION NUMBER: 94810746.1
EARLIER FILING DATE: 1994-12-22
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EARLIER APPLICATION NUMBER: 08/860,150
EARLIER FILING DATE: 1997-06-19
                                                                                                                       AATCGACGCCCTCGCCTACAGCACC
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Patent No. 6040164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 49.9
Matches 539; Conservative
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; LOCATION: (132)..(1499)
US-09-338-132-1
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                                                                                          APPLICANT: Millward, Thomas A.
TITLE OF INVENTION: Nuclear DBF2-Related (NDR) Kinases
FILE REFERENCE: 4-20265/A/PCT
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Pred. No. 4.
                                                                                                                                                                CURRENT APPLICATION NUMBER: US/08/860,150B
CURRENT FILING DATE: 1997-06-19
EARLIER APPLICATION NUMBER: PCT/EP95/05052
EARLIER FILING DATE: 1995-12-20
                                                                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: 94810746.1
Sequence 1, Application US/08860150B
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Drosophila melanogaster
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NUMBER OF SEQ ID NOS:.18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
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Best Local Similarity 49.9
Matches 539; Conservative
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; LOCATION: (132)..(1499)
US-08-860-150-1
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Search completed: January 16, 2003, 21:55:17 Job time: 162.058 secs

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January 16, 2003, 09:56:42; Search time 110.556 Seconds (without alignments) 16067.254 Million cell updates/sec
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'pubpna/US08_PUBCOMB.seq:'
'pubpna/US09_NEW_PUB.seq:'
'Apubpna/US09_PUBCOMB.seq:'
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                         393868 seqs, 222934149 residues
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Maximum Match 100%
Listing first 45 summaries
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                                                                                          OM nucleic - nucleic search, using sw model
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Pred. No. is, the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result	2	Query				
No.	Score	Match	Match Length DB	ОВ	QI	Description
-	655.4	16.5	2043	5	US-09-836-392-2	Sequence 2, Appli
c 5.	609.8	15.3	638	10	US-09-879-536-26	Sequence 26, Appl
٣	452.8	11.4	678	10	US-09-879-536-66	Sequence 66, Appl
4	346.2	8.7	929	φ	US-09-764-868-214	Sequence 214, App
2	261.4	9.9	1689	δ	US-09-938-842A-1861	Sequence 1861, Ap
9	254.6	6.4	3583	6	US-09-974-298-152	
7	216.8	5.4	1452	σ	US-09-938-842A-2402	Sequence 2402, Ap
8	186	4.7	734	σ	US-09-764-868-196	, F4.
σ	171.8	4.3	1818	10	US-09-771-161A-89	Sequence 89, Appl
10	122.8	3.1	2706	12	US-10-071-751-20	
11	120.6	3.0	1416	6	US-09-938-842A-2503	~
. 12	120.2	3.0	5313	10	US-09-801-368-297	
13	119.2	3.0	1398	6	US-09-938-842A-633	٩.
14	117	2.9	268	6	US-09-796-692-8122	Sequence 8122, Ap
15	117	2.9	6409	10	US-09-864-864-293	Sequence 293, App
16	116.2	2.9	2637	10	US-09-799-875-3	Sequence 3, Appli
17	116.2	2.9	3003	10	US-09-799-875-1-	Sequence 1, Appli
18	112.6	2.8	2365	6	US-09-981-353-6	Sequence 6, Appli
. 19	112.4	2.8	277	10	US-09-294-093B-2043	Sequence 2043, Ap

Sequence 38, Appl	Sequence 37, Appl	4	Sequence 6, Appli	Sequence 1, Appli	Sequence 214, App	Sequence 3855, Ap	Sequence 217, App	Sequence 399, App	Sequence 46, Appl	Sequence 1, Appli	Sequence 3, Appli	1,	41,	Sequence 570, App	Sequence 403, App	Sequence 1137, Ap	Sequence 3, Appli		1,	$^{\circ}$	ď,	Sequence 3691, Ap	Sequence 1978, Ap	Sequence 7789, Ap	Sequence 2146, Ap	
10 US-09-771-161A-38	10 US-09-771-161A-37	9 .US-09-764-868-58	10 US-09-810-808-6	9 US-10-000-039-1	10 US-09-969-347-214	10 US-09-880-107-3855	9 US-09-764-868-217	10 US-09-801-368-399	10 US-09-771-161A-46	_	12 US-10-028-946-3	12 US-10-028-946-1	9 US-09-954-531-141	9 US-09-954-531-570 .	10 US-09-801-368-403	10 US-09-954-456-1137	9 US-10-017-216-3	9 US-10-017-216-1	10 US-09-784-249-1	10 US-09-801-368-401	9 US-10-098-841-195	10 US-09-880-107-3691.	9 US-09-938-842A-1978	9 US-09-796-692-7789	10 US-09-880-107-2146	
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112.4	112.4	111.6	111	111	111	111	107.4	106.4	105.2	101.4	101.4	101.4	100.4	100.4	66	98.2	96.6	9.96	95	93.4	93.4	93.6	92.2	91.4	91.4	
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## ALIGNMENTS

KESULY I IRC-09-836-302-2
Sequence 2. Application US/09836392
; Patent No. US20020173458A1
GENERAL INFORMATION:
** AFTILEAN: NUCCH EL 21. ** AFTILE OF INVENTION: Protein Turcaine Kinase Recentor Dolumicleotides. Polumentides
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: PT020P1
; CURRENT APPLICATION NUMBER: US/09/836,392
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/165,914
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/189,027
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2043
TYPE: DNA
; ORGANISM: Homo sapiens
US-09-836-392-2
æ.
Pred. No. 1.6e-148;
O; Mismarches 401; Indels 3; Gaps
QY 2241 GTTGGATTATCTCAAGATGCCCAGGATCAAATGAGAAGATGCTTTGCCAAAAAGAATCT 2300
Dh
OY 2301 AATTACATCCGTCTTAAAAGGGCTAAAATGGACAAGTCTATGTTTGTGAAGATAAAGACA 2360
Db 278 AATTACAACAGGTTAAAGAGGGCCAAGATGGACAAGTCTATGTTTGTCAAGATCAAAACC 337
OY 2361 CTAGGAATAGGAGCATTTGGTGAAGTCTGTCTAGCAAGAAAAGTAGATACTAAGGCTTTG 2420
Db 338 CTGGGAPCGGTPTGGAGAAGGGCCTFTGT
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                                                      TCATTCCAAGATAAGGACAATTTATACTTTGTAATGGACTACATTCCTGGGGGTGATATG
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           ATGAGCCTATTAATTAGAATGGGCATCTTTCCAGAAAGTCTGGCACGATTCTACATAGCA
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3501 TATAATTATCCGAAGCCTATTGAATATGAATACATTAATTCACAAGGCTCAGA 3553
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                       1475 TITCGAIGCCCAAAGCCITCAGGAGCAGGAAGCTTCACAGGCIGAGAGCTCAGA
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                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION TITLE OF INVENTION: PRODUCTS FILE REFERENCE: CCD-257 (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 609.8; DB 10
Pred. No. 9.2e-138;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/879,536 CURRENT FILING DATE: 2001-09-21
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/088,801
                                                                                        Sequence 26, Application US/09879536 Patent No. US20020144298A1
                                                                                                                                                                  Burgess, Christopher C
Bushnell, Steven E.
Carroll III, Eddle
Catino, Theodore J.
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Astle, Jon H.
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98.4%;
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                                                                                                                                                                                                                                           Lewis, Marcia E.
Monahan, John E.
Schlegel, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 98.4 Matches 627; Conservative
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US-09-879-536-26
                                                                                                                     GENERAL INFORMATION:
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APPLICANT:
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2714 TATTAAACCTGATAATATTTTGATC--GTGATGGTCATATTAAATTGACTGACTTT 2771
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   TTCATTCCAAGATAAGGACAATTTATACTTTGTAATGGACTACATTCCTGGGGGTGATAT
                                                                                                                                              2600 GATGAGCCTATTAATTAGAATGGGCATC-TTTCCAGAAAGTCTGGCACGATTCTACAT--
                                                                                                                                                                                                                    2657 AGCAGAACTTACCTGTG-CAGTTGAAAGTGTTCATAAAA--TGGGTTTTATTCATAGAGA
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Pred. No. 4.7e-74;
2; Mismatches 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 214, Application US/09764868
Patent No. US20020168711A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PT232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/764,868 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: n equals a,t,g, or C US-09-764-868-214
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Best Local Similarity 71.2
Matches 481; Conservative
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2658 GCAGAACTTACCTGTGCAGTTGAAAGTG -- - TTCATAAAATGGGTTTTATTCATAGAGAT 2714
                                                                      2240 GGTTGGATTATCTCAAGATGCCCAGGATCAAATGAGAAAGATGCTTTGCCAAAAAGAATC 2299
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APPLICANT: Lewis, Marcia E.
APPLICANT: Mondheal, John E.
APPLICANT: Scholbert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
FITLE OF INVENTION: PRODUCTS
FILLE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/879,536
PRIOR RELIGION NUMBER: US 60/088,801
PRIOR FILING DATE: 1998-06-10
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Pred. No. 8.2e-100;
                                                                                                                                            2775 CTCTGCACTGGCTTCAGATGGACACGATTCTAAGT 2811
                                                                                                                                                               NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 66
                                                                                                                                                                                                                                                                   Sequence 66, Application US/09879536
Patent No. US20020144298A1
GENERAL INFORMATION:
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LOCATION: (1). ...(678)
OTHER INFORMATION: n = A,T,C or G
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Bushnell, Steven E.
Carroll III, Eddie
Catino, Theodore J.
Derti, Adnan
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Astle, Jon H.
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90.1%;
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Best Local Similarity 90.1
Matches 548: Conservative
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ORGANISM: Homo sapiens
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RESULT 6
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                                                                                                                                                                                                                                                   888 GIICATAAAAIGGGIITITAIICAIAGAGAIAITAAACCIGAIAAIAIIIIGAIIGAICGI 2744
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420 TACTITGTGATGGACTACATCCCTGGTGGGGACATGATGACCTGCTGATCCGGATGGAG
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                                                                               361 GAGGCAGACAATGAGTGGGT-GGCAAACTCTACTACTCCTTCCAAGACAAAGACAGCCTG
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PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1861, Application US/09938842A Patent No. US20020160378A1
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ilarity 52.7%;
Conservative
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Wang, Xun
Zhu, Tong
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Matches 642; Conserv
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09-938-842A-1861
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                                                                                                                                                                                                                                                     2561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTGATGGTCATATTAAATTGACTGACTTTGGCCTCTGCACTGGCTTCAGATGGACACAC 2801
337 CAGAAAATGGGGGGTTGATGACTTTGAACTGCTTAGCATCATTGGCCGGGGTGCTTTCGGT 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3161 CAGTCCTGAAGCTTCTGATCTTATTATAAACTTTGCCGAGGACCCGAAGATCGCTTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3101 AACACAAATGAAGGTTATCAACTGGCAAACATCTCTTCACATTCCACCACAAGCTAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             637 GATACCTTACGGGAAGATGAGACTCGGTTTTATGTTGCGCAGACAATTCTGGCTATTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1050 AGCAATCATGTTCGGGATGCTTGTAGGGTTTCCGCCATTCTATTCCGAAGAACCTTTGGC
                                                  2382 GAAGTCTGTCTAGCAAGAAAGTAGATACTAAGGCTTTGTATGCAACAAAAACTCTTCGA
                                                                                                     397 GAGGTGAGAATTTGTAAAGAAAATCTACTGGAAGCGTATATGCAATGAAAAGTTAAAAG
                                                                                                                                                                                                                                                        697 TCTATCCATAAGCATAATTACGTCCACAGGGATATAAAAGCCTGATAATTATTGATTACT
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                                                                                                                                                     AAGAAAGATGTTCTTCGAAATCAAGTCGCTCATGTTAAGGCTGAGAGATATCCTG
                                                                                                                                                                                                  GGCATCTTTCCAGAAAGTCTGGCACGATTCTACATAGCAGAACTTACCTGTGCAGTTGAA
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1067 ATGAATTCCAAAAG-
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| 1514 GAT 1516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CANATGAGAAAGATGCTTTGCCAAAAAGAATCTAATTACATCCGTCTTAAAAGGGCTAAA
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                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID NO. US20020156263A1 347975.11
-09-974-298-152
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                             GENERAL INFORMATION:
APPLICANT: Chen, Huei-Mei
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                       DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 519;
                                                                                                                                                                                                                                                                                                                                                                                          No. 1.6e-
                                                                              FILE REFERENCE: PA-0037 P
CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR FILING DATE: 2000-05-10
NUMBER: OF SEQ ID NOS: 194
SEQ ID NO 152
                                                                                                                                                                                                                                                                                                                                                                       Score 254.6;
ce 152, Application US/09974298
No. US20020156263A1
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                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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                                                                                                                                                                                                                              LENGTH: 3583
                                                                                                                                                                                                                                                                                                                                                                                        Best Local Sim
Matches 645;
 Sequence 152,
                                                                                                                                                                                                                                               TYPE: DNA
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APPLICAMY: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SARE, AND METHODS OF USE
TITLE OF INVENTION: SARE, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT PILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR PLING DATE: 2000-08-24
PRIOR PLING DATE: 2000-08-24
PRIOR PLING DATE: 2000-08-16
PRIOR PLING DATE: 2001-01-16
PRIOR PLING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION UNMER: US 60/300,111
NUMBER OF SEQ ID NOS: 5379
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                                                                                                                                                                                                                                                                                                       3108 ATGAAGGTTATCAACTGGCAAACATCTCTTCACATTCCACCACAAGCTAAACTCAGTCCT 3167
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                                                                  -GAAAGCAGAAACCTGGA 1097
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2868 GGGGATCCCTCAAGCTGTCGATGTGGAGACAGACTGAAGCCATTAGAGCGGAGAGCTGCA
                                                                                                                                                                   2988 GAAGIGTIGCTACGAACAGGATACACACAGTIGTGTGATIGGTGGAGTGTIGGTGTTATI
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TGGGTAGTTCGTCTATATTATTCATTCCAAGATAAGGACAATTTATACTTTGTAATGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                        TACATTCCTGGGGGTGATATGATGAGCCTATTAATTAGAATGGGCATCTTTCCAGAAAGT
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                                                                     277 GACTITGAGCTTTTGACTATCATTGGAAGAGGTGCTTTTGGTGAGGTTCGCTTATGTCGG
                                                                                                                                                             GAGAGAAAGTCTGGAAATATTTATGCCATGAAGAAGTTAAAAGAAATCTGAAATGGTCATG
                                                                                                                                                                                                                                                     CGAAATCAAGTCGCTCATGTTAAGGCTGAGAGAGATATCCTGGCTGAAGCTGACAATGAA
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                                                                                                                                                                                                                                                                                                                                                Length 734;
                                                                                                          and Antibodies
                                                                                                                                                                                  file

    refer to,PALM or

                                                                                                                                                                                                                                                                                                                                                  Score 186; DB 9;
Pred. No. 2.5e-35;
2; Mismatches 297;
                           Sequence 196, Application US/09764868
Patent No. US20020168711A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REPERENCE: PT23
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    432 AATCTCACACACACCCACCAAGT ---
                                                                                                                                                                                Prior application data removed
NUMBER OF SEQ ID NOS: 1510
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 196
                                                                                                                                                                                                                                                                                                                                                  4.7%;
ilarity 55.6%;
Conservative
                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 419; Conserv
RESULT 8
US-09-764-868-196
                                                                                                                                                                                                                                                                                                                 US-09-764-868-196
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2748 GGTCATATTAAATTGACTGACTTTGGCCTCTGCACTGGCTTCAGATGGACACACGATTCT 2807
                                                              1264 GGCCATGTGAAACTTTCTGACTTTGGTCTTTGCACAGGACTGAAAAAAGCACATAGGACA 1323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weber, Eric R.
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS AND APPARATUS TO COLLECT SUCH PROTEINS
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Pred. No. 9.5e-20;
0; Mismatches 182; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-17-C4-PUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: SHERIDAN ROSS P.C. STREET: 1560 BROADWAY, SUITE 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/071,751
FILING DATE: 07-Feb-2002
CLASSIFICATION: <a href="color: blue;">CLASSIFICATION: <a href="color: blue;">COLASSIFICATION: blue;</a></a>
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; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-071-751-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/171,156
FILING DATE: 1998-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                      1324 GAATTTTATAGGAATCTGAACCA 1346
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hunter, Shirley Wu
                                                                                                                          2808 AAGTACTATCAGAGTGGTGACCA 2830
                                                                                                                                                                                                                                                                                                                                       Sequence 20, Application US/10071751
Patent No. US20020142352A1
GENERAL INFORMATION:
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TELEFAX: 303/863-0223
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STRANDEDNESS: single
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Best Local Similarity 57.0%;
Matches 245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sim, Gek-Kee
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MEDIUM TYPE: Flopp
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ZIP: 80202
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                                                                                                                                                                                                                                                                                                          US-10-071-751-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2208 CGTAAAAAACAATTAGAGAATGAAATGATGCGGGTTGGATTATCTCAAGATGCCCAGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2328 ATGGACAAGTCTATGTTTGTGAAGATAAAGACACTAGGAATAGGAGCATTTGGTGAAGTC
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Pred. No. 1.1e-31;
); Mismatches 312;
                                                                                                                                                                                                                                                                                              APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: 0S/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR PAPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
3120 AACTGGCAAACATCTCTTCACATTCCACCACAAG 3153
                            696 AACTGGAAAGAACTCTGGTATTTCCTCCAGAGG
                                                                                                                                                                                                            Sequence 89, Application US/09771161A Patent No. US20020110811A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: Patentin version 3.0
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al Similarity 54.2%;
370; Conservative
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dden, Kevin
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                                                                                                                                                                                                                                                                                                                                     Peter
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                                                                                                                                                                                                                                                                                                                                                                                Maxon, Mary
                                                                                                                                                                      838 ACTGATTTTG 848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Va.
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; ORGANISM: Sac
US-09-801-368-297
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                                                                                                                                                                                                                                              US-09-801-368-297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 5313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2403 GTAGATACTAAGGCTTTGTATGCAACAAAAACTCTTCGAAAGAAGAAGATGTTCTTCTTCGA, 2462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATTAATTAGAATGGGCATCTTTCCAGAAAGTCTG .2642
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                                                                                                                1592 GGTGATATGATGAGCCTATTAATTAGAATGGGCATCTTTCCAGAAAGTCTGGCACGATTC 2651
                                                                                                                                                                         TACATAGCAGAACTTACCTGTGCAGTTGAAAGTGTTCATAAAATGGGTTTTATTCATAGA 2711
                                                                                                                                                                                                                                   192 TATACAATGGAAGTGGTGCTAGCACTTGATACAATTCACTCCATGGGATTTGTACATCGT 451
                                                                                                                                                                                                                                                     335 GGTGACTTGGTGAGTCTTATGTCCGATTATGAAA---TTCCAGAAAAATGGGCAATGTTC 391
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               2532 CTATATTATTCCAAGATAAGGACAATTTATACTTTGTAATGGACTACATTCCTGGG
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Pred. No. 2.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -REGULATED GENES OF AND METHODS OF USE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ICATION NUMBER: US/09/938,842A
ING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2000-08-24 APPLICATION NUMBER: US 60/264,647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATION NUMBER: US 60/227,866
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2503, Application US/09938842A Patent No. US20020160378A1
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illarity 55.0%;
Conservative 0
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CURRENT APPLICATION NUMBER: (
CURRENT FILING DATE: 2001-08
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                                                                                                                                                                                                                                                                                                   2772 GGCCTCTGCA 2781
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US-09-938-842A-2503
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OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
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                                               718 GCTCGTGTGTACACTGCAGAAATCGTCTCTGCAGTTTCCCATCTCCATGAGAAAGGCATA 777
                                                                                                                                        2450 GAGATTATTTTGCTATAAAGGTTCTAAGGAAATCAGATATGATTGCCAAAAATCAAGTAA
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2643 GCACGATTCTACATAGCAGAACTTACCTGTGCAGTTGAAAGTGTTCATAAAATGGGTTTT
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Best Local Similarity 56.6%; Pred. No. 5.8e-19;
Matches 243; Conservative 0; Mismatches 183;
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RIOR FILING DATE: 2000-01-19
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2650 TCTACATAGCAGAACTTACCTGTGCAGTTGAAAGTGTTCATAAAATGGGTTTTATTCATA 2709

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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THEY TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
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Score 117;
Pred. No. 1
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APPLICATION NUMBER: 60/200,545
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APPLICATION NUMBER: 60/218,950
                                                                                                                                                                                                                                                                                                    NT FILING DATE: 2001-03-01 APPLICATION NUMBER: 60/186,126
                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2000-03-01 APPLICATION NUMBER: 60/190,479
                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2000-04-27
APPLICATION NUMBER: 60/200,303
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APPLICATION NUMBER: 60/200,779
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APPLICATION NUMBER: 60/200,999
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Best Local Similarity 56.2%;
Matches 241; Conservative
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APPLICATION NUMBER: 60/
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                                                                                                                                                                       APPLICANT: Gaiger, Alexander
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NAME/KEY: unsure
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US-09-796-692-8122
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE
                                                                 2750 AIGACTTAAAGCCTGAAAATCTACTAATTGATAATGCAGGTCATGTGAAATTAAAGAGATT 2809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2322 GCTAAAATGGACAAGTCTATGTTTGTGAAGATAAAGACACTAGGAATAGGAGCATTTGGT 2381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2382 GAAGTCTGTCTAGCAAGAAAGTAGATACTAAGGCTTTGTATGCAACAAAAACTCTTCGA 2441
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Pred. No. 5e-19;
0; Mismatches 208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 633
                                                                                                                                                                                                                                                        -09-938-842A-633
Sequence 633, Application US/09938842A
Patent No. US20020160378A1
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Best Local Similarity 54.0%;
Matches 244; Conservative
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Zhu, Tong
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                                                                                             ACATAGCAGAACTTACCTGTGCAGTTGAAAGTGTTCATAAAATGGGTTTTATTCATAGAG 2712
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                                                          ; DB 10; Length 6409; 3.8e-18;
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                                                                                                                                                                                                                                                                                                           Sequence 293; Application US/09864864
Patent No. US20020102679A1
GENERAL INFORMATION:
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Best Local Similarity 56.2%;
Matches 241; Conservative
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arlocker, Susan I
illon, Davin C.
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Lodes, Michael J.
Algate, Paul A.
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US-09-864-864-293
                                                                                                                                                                                                               2773 GCCTCTGCA 2781
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                                                                                                                                                                                                                                         443 GCACGTGTA 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ I
SOFTWARE: Corix
SEQ ID NO 293
LENGTH: 6409
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US-09-864-864-293
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1035 ACATGCTGAAGTTCTTGCTCTGGAAGTGTTCATAAAATGGGTTTTATTCATAGGG 2712

Db 1035 ACATGCTGAAGTTCTTTGGTTGGAAGAATACACTCCATGGGTTTAATACAGGG 1094

OY 2713 ATATTAAACTGATAATTTTGATTGATGGTCATATTAAATTGCTGATTTG 2772

Db 1095 ATGTGAAGCTGACAACATGCTCTTGGATAAAATTAGCAGATTTTG 1154

OY 2773 GCCTCTCA 2781

Db 1155 GCACGTA 1163

Search completed: January 16, 2003, 22:02:57

Job time: 183.556·secs
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4), (\*)

7: gb_gss:* LOCUS  8: em_gss_hum:* DEFINITION  9: em_gss_inv:* ACÇESSION  00: em_gss_pln:* VERSION  11: em_gss_vrt:* KEYWORDS  22: em_gss_fun:* SOURCE
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BM950668 UI-M-EHOP BE08834 CAMI-EF068 B0312644 MR0-BN011 BQ291582 PM3-AN002 AM642458 CM19a02.w AM642458 CM19a02.w BB751204 BB751204

BQ201853 UI-R-DO1-BG081236 H3062G12-BE395243 601311110

BQ898648 AGENCOUR vol5f09.y

A1594372

AGENCOURT H3064C02-

ut60q11.

AIS96344 me57h09.x BI331257 602982912 AA592233 vo15f09.r BE620135 601483053 BF396283 UI-R-BS2-BI664597 603290249

ALIGNMENTS

Description AF119846 Homo sapi BC015665 Homo sapi A7114863 HA1474 Hu AV708169 AV708169 BM971435 UI-CF-DUI	,
Descr AF11 BC01 AI114 AV7C BM97	1
SUMMARIES SUMMARIES SUMMARIES SUMMARIES SUMMARIES SECONDES SUMMARIES SUMMARI	
08 111 111 110 114	1
Query  Query  Match Length DB ID  23.4 1807 11 AF1  20.2 1216 11 BCO 17.5 721 9 A111 16.3 694 10 AV7 14.8 657 14 BM9 14.1 203 1843	-
Ouery Match 23.4 20.2 17.5 16.3	! ! !
Score 930.8 804.8 697.4 650.8 550.6	
ult No. 1 2 3 3 4	,
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linear HTC 08-MAY-2001. 2 (bases 1 to 1807)
Zhang,C., Yu,Y., Zhang,S., Wei,H., Zhang,Y., Zhou,G., Bi,J., Liu,M. Zhang, S., Wei, H., Zhang, Y., Zhou, G., Bi, J., Liu, M. Direct Submission Submission Submitted (13-JAN-1999) Department of Experimental Hematology, Institute of Radiation Medicine, Beijing Taiping Road 27, Beijing, Beijing 100850, P. R. China Location/Qualifiers oa; Chordata; Craniata; Vertebrata; Euteleostomi; ia; Primates; Catarrhini; Hominidae; Homo. 807) ction of the coding sequences of 79 new genes sis of cDNA clones from human fetal liver 1474 mRNA, complete cds. MRNA 1. .1807 /organism="Homo sapiens /db\_xref="taxon:9606" /clone="FLB5626" 1807 bp 770128 source REFERENCE AUTHORS TITLE JOURNAL FEATURES

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HTC 09-0CT-2001

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Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R., Lim, M., Maduro, Q.L., Masiello, C., Mastrian, S.D., McCloskey, J.C., Tiongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                             Homo sapiens, Similar to LATS (large tumor suppressor, Drosophila) monolog 1, clone IMAGE:4550430, mRNA. BC015665.1 GI:15990533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (04-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                       154 TTAGTTCCTCAGAGGCATGGCCCGCCACTAGGAGAAAGTGTGGCCTATCATTCTGAGAGT
                                     843 CCCAACTCACAGACAGATGTAGGAAGACCTTTGTCTGGATCTGGTATATCAGCATTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nisc_mgc@nhgri.nih.gov
                                                                                                                903 CAAGCTCACCCTAGCAACGGACAGAGAGTGAACC 936
                                                                                                                                                   CAAGCTCACCCTAGCAACGGACAGAGGGAACC 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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BC015665
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RRRWPGVKGRARSLRPLGRAALARGSPPVRLPALPHQGYLGLLGRTLAASASALRPVA
                                                                                                                                   /translation="MADKLSDRVFKASYTFQEVHVFIQGLPEGLEMAGLQQVPEVQNL
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                                                                                                                                                                                                                                                                                     8; DB 11; Length 1807;
4.1e-228;
thes 2; Indels 0;
                       complement(841. .1530)
/note="predicted protein of HQ1474"
                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                  /protein_id="AAF69600.1"..
/db_xref="G1:7770129"
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found
                                                                                      This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10862687 This clone has the following problem: incomplete processing.
Clone distribution: MGC clone distribution information can be for
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 33 Row: b Column: 11
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                                                                                                                                                                                                                                                                                                                              /tissue_type="Lung, large | /clone_lib="NIH_MGC_18" | /lab_host="DH10B-R" | /lab="Vector: p0TB7" | 270 c | 251 g | 280
                                                                                                                                                                                                                                          /organism="Homo sapiens"
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/clone="IMAGE:4550430"
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ACCESSION A1114863 VERSION A1114863.1 GI:6360208	EST. human. Homo sapi	Mammalia; Eutheria; Prime REFERENCE 1 (bases 1 to 721) AUTHORS Yu,Y., Zhang,C., Luo,L., and He.F.	TITLE Expression profile analys JORNAL Unpublished (1998) , COMMENT Contact: Yongtao Yu Department of Hematology	Beijing Institute of Radi 27 Taiping Road, Beijing Tel: 0086-10-68159479 Fax: 0086-10-68214653	Email: yyt48@yahoo.com. FEATURES Location/Qualifi source 1.721 /organism="Homo	/db_xref="taxon: /clone_lib="Huma /tissue_type="li" /dev_stage="feta	/lab_host="MC106 /note="vector: F ORIGIN 170 a 156 c 151	Query Match 17.5%; Scc Best Local Similarity 98.8%; Pre Matches 712; Conservative 0;	OY 217 ATATAGATGTTTTCATGAAGAGGAGTG	Qy 277 AGACCTTTCCTG-CCAGTAACTATACT 	336	Db 601 GAATCCCTTAGGAATTTATCTAAACCA Qy 396 AAAATGTCAACGAAGATCCTCGACAA	541	Qy 456 AAAGCCTTGCAGGAAATTCGAAACTTT	Qy 516 CGGAGTACTTCAGAAGTTAATCCACAA	Oy 576 GAGGATATGGTTATACAAGCTCTTCAG	OY 636 GAATTCATTAGTAAAATGAGTTACCAA 	QY 696 GCCAGACCTATTAATGCCAGCATGAAA	Oy 756 CAGAGCTGGAAAGGTTCTAAAGAATCC
Db 98 CTTGGGGTTGCTGGACGACTCTGGCCGCCTCAGCGCCCTCAGGCCCGTGGCCGC 157	Qy         63         TGTCCAGGAGCTCTGCTCCCCTCCAGAGTTAATTTATATTGTAAAGAATTTAAC         122           .	OY 123 AGTCCTGGGACTTCCTTGAAGGATCATTTTCACTTTTGCTCAGAAGAAAGCTCTGGATC 182	   Tatcaataaagaagiccttcgtgtgggctacatatatagatgtttcatgaagagagt 	OY 243 GAAAAGCCAGAAGGATATAGACAAATGAGGCCTAAGACCTTTCCTGCCAGTAACTATACT 302 	OY 303 GTCAGTAGCCGGCAAATGTTACAAGAAATTCGGGAATCCCTTAGGAATTTATCTAAACCA 362 	Oy 363 TCTGATGCTGCTAAGGCTGAGCATAACATGAGTAAAATGTCAACCGAAGATCTCGGCAA 422 	OY 423 GTCAGAAATCCACCCAAATTTGGGACGCATCATAAAGCCTTGCAGGAAATTCGAAACTCT 482 	OY 483 CTGCTTCCÀTTGCAAATGAAATTCTTCTCGGAGTACTTCAGAAGTTAATCCACAA 542 	QY 543 ATGCTTCAAGACTTGCAAGCTGCTGGATTTGATGAG	Qy 579 578 Db 698 тсасссатфатентаставаессаттентававансностинававане 257	579	Db 758 CTCTAGGACAAGATATGGTTATACAAGCTCTTCAGAAAACTAACAACAGAAGTATAGAAG 817 Qy 628 CAGCAATTGAATTCATTAGTAAAATGAGTTACCAAGATCCTCGACGAGAGAGA	818 CAGCAATTGAATTCATTAGTAAAATGAGTTACCAAGATCCTCGACGAGAGCAGGATGGCTG	Oy 688 CAGCAGCTGCCAGACCTATTAATGCCAGCATGAAACCAGGGAATGTGCAGCAATCAGTTA 747	OY 748 ACCGCAAACAGAGCTGGAAAGGTTCTAAAGAATCCTTAGTTCCTCACAGGCATGGCCGC 807	OY 808 CACTAGGAGAAAGTGTGGCCTATCATCAGAGTCCCAACTCACAGCAGATGTAGGAA 867 	OY 868 GACCTTTGTCTGGATCTGGTATATCAGCATTTGTTCAAGCTCACCCTA 915 		LOCUS A114863 721 bp mRNA linear EST 11-NOV-1999 DEFINITION HA1474 Human fetal liver cDNA library Homo sapiens cDNA, mRNA sequence.
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rdata; Craniata; Vertebrata; Buteleostomi;
mates; Catarrhini; Hominidae; Homo.
                                , Ouyang, S., Li, W., Wu, J., Zhou, S., Liu, M.
                                                    ysis of a human fetal liver cDNA library
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	CAGAGCTGGAAAGGTTCTAAAGAATCCTTAGTTCCTCAAGGGGTGGGCCCCCCCC			0.1	-	AV/08L09 AUC HOMO Saprems Com Cross Av/08L09 AV708L69.1 GI:10725434 EST.	numan. Homo sapiens Eukaryota; Metazoa;		Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu Zeng, K., Chen, J., Chen, Z. and Han, Z.		Chine 351 G 20120	Tel: 8-21-50801919(ex.45) Fax: 86-21-50801922 Email: hanzqebng:sh.cn	-		/clone_lib="ADC" /tissue_type="Adrenal gland" /dev_stage="Adult"	/lab_nost=_solnk /note="Vector: pB Xho!"	229 a 1// C 124 9 102 C 200020	Query Match 16.3%; Score 650.8; DB 10; Length 694; Best Local Similarity 97.8%; Pred. No. 3.5e-156; Matches 680; Conservative 0; Mismatches 13; Indels 2; Gaps	7 GTCATAACATGGAACTATAACATTAGTGTACCTGGACTGCAAACAAA	37 CATCTTCTGCTCCAGCCCAGTCATCCCCGAGCAGTGGGCATGAAATCCCTACATGGCAAC 1596		7 CIGCTAATICICAGCCTICIGCTACAACAGTCACIGCAATIACACCAGCICCTATICAAC 1716
-	Db 181 Qy 816		o,	Db 1	RESULT 4 AV708169 LOCUS	DEFINITION ACCESSION VERSION KEYWORDS	SOURCE	REFERENCE AUTHORS		TITLE JOURNAL			FEATURES		,		BASE COUNT ORIGIN	Query Ma Best Loo Matches	Oy 1477 Db 1	Oy 1537 Db 61	1	Oy 1657

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1-mccray@ulowa.edu
urmement: Dr. M. J. Welsh, University of Iowa
ury preparation: Dr. M. Bento Soares, University of Iowa
nry preparation: Dr. M. Bento Soares, University of Iowa
nry Arrayed by: Dr. M. Bento Soares, University of Iowa
ncing by: Dr. M. Bento Soares, University of Iowa
nribution: Researchers may obtain clones from Research
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ng. respectitive elements were found in this cDNA
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                                                                                                                                                                            CTGTGATGCCACCTGTTGCTGAAGCTCCAAACTATCAAGGACCAC 1896
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Itheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Iowa Med Labs, Iowa City, IA 52242, USA
                                                                                                                           , Lennon, G. and Soares, M.D. and subtraction: two approaches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lennon, G. and Soares, M.B.
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                                                       /Jab_host="DAHOB (Life Technologies) (T1 phage resistant) "Inchest="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-CF-DUI is a normalized CDNA library containing the following tissue(s): Primary Lung Epithelial Cells The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dr primer containing a Not I site Double stranded CDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (GT)8 tail. The sequence tag for this
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TAG_LIB=UI-CF-DUI
TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2131 ATTCTCCTCAAGCATTTAAATTCTTTATGGAGCAACATGTAGAAAATGTACTCAAATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 ATTCTCCTCAAGCATTTAAATTCTTTATGGAGCAACATGTAGAAAATGTACTCAAATCTC
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                                                                                                                                                                                                                                                                                                                                                                                       DB 14; Length 657;
/clone="U1-CF-DU1-abd-1-16-0-U1"
/clone_lib="U1-CF-DU1"
/tissue_type="Primary Lung Epithelial Cells"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                   Score 590.6; DB 14;
Pred. No. 1.1e-140;
0; Mismatches 25;
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                                                                                                                                                                                                                                                                                                                          TAG_SEQ=GGCTGTAGGC
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Best Local Similarity 96.0%;
Matches 605; Conservative
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/tissue_type="large cell carcinoma"
/Lissue_type="large cell carcinoma"
/Lib host="DH108 (phage-resistant)
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI, CDNA made by oligo-dT priming. Directionally cloned
into ECORIXADI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Supersoribt II RT (Life Technologies). Note: this is a
NIL MGC Library
272 c 281 g 320 t
HG1312628FI NIH_MGC_18 HOMO sapiens cDNA clone IMAGE:4550430 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó;
                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122
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                                                                                                                                                                                                                                                                                                                                                               National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 CTTGGGGTTGCTGGGACGGACTCTGGCCGCCTCAGCGTCCGCCCTCAGGCCCGTGGCCGC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 AGTCCTGGGGACTTCCTTGAAGGATCATTTTCACTTTTGCTCAGAAGAAAGCTCTGGATC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 AGTCCTGGGGACTTCCTTGAAGGATCATTTTCACTTTTGCTCAGAAGAAAGCTCTGGATC 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAAAGCCAGAAGGATATAGACAAATGAGGCCTAAGACCTTTCCTGCCAGTAACTATACT 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 GTCAGTAGCCGGCAAATGTTACAAGAAATTCGGGAATCCCTTAGGAATTTATCTAAACCA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 TATCAAATAAAGAAGTCCTTCGTGTGGGCTACATATATAGATGTTTTCATGAAGAGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 GAAAAGCCAGAAGGATATAGACAAATGAGGCCTAAGACCTTTCCTGCCAGTAACTATACT
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Pred. No. 1e-132;
); Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://mage.lln.gov
Plate: LLCM1243 row: g column: 07
High quality sequence stop: 724.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="NIH_MGC_18"
                                                                                                                                                                                                                                                                                                            1 (bases 1 to 1203)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone="IMAGE:4550430"
                                                                                                                      BG331628.1 GI:13138066
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98.3%;
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Best Local Similarity 98.3
Matches 566; Conservative
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3200

3259

460

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400

3379

RESULT 7 AA910802/c

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LOCUS

ACCESSION

VERSION KEYWORDS

SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL

COMMENT

3499

3559

390 363 450 423 510 483 570

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Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Magal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jorgeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was derived from the FAPESP/LICR Human Cancer Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
                             3081 TTGGCACAAACACCATTAGAAACACAAATGAAGGTTATCAACTGGCAAACATCTCTTCAC 3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3560 GTCGGATGAAGATGATCAAAACACAGGCTCAGAGATTAAAAATCGCGATCTAGTATATGT 3619
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                                                                                                                                                                                                                       3201 GGACCCGAAGATCGCTTAGGCAAGAATGGTGCTGATGAAATAAAAGCTCATCCA-TTTTT
                                                                                                                                                                                                                                                                                                                3260 TAAAACAATTGACTTCTCCAGTGACCTGAGACAGCAGTCTGCTTCATACATTCCTAAAAT
                                                                                                                                                                                                                                                                                                                                            399 TAAAACAATTGACTTCTCCAGTGACCTGAGACAGCAGCTGCTTCATACATTCCTTAAAAT
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                                                                                                                           3141 ATTCCACCACAAGCTAAACTCAGTCCTGAAGCTTCTGATCTTATTAAAACTTTGCCGA
                                                                                                                                                                                                                                                  .3500 ATATAATTATCCGAAGCCTATTGAATATGAATACATTAATTCACAAGGCTCAGAGCAGCA
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Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 578)
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BE093083
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 13-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 637)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 415.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3021 TGTGATTGGTGGAGTGTTGGTGTTATTCTTTTTGAAATGTTGGTGGTGGGACAACCTTCTTTTC 3080
                                                                                                482
                                                                                                                                                                                                                     569
                                                                                                                                                                                                                                                               CTGCTTCCATTTGCAAATGAAACAAATTCTTCTCGGAGTACTTCAGAAGTTAATCCACAA 542
                                                                                                                                                                                                                                                                                        CTGCTTCCATTTGCAAATGAAACAAATTCTTCTCGGAGTACTTCAGAAGTTAATCCACAA 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ol48d06.sl Soares_NFL_T_GBC_Sl Homo sapiens cDNA clone IMAGE:1526699 3' similar to TR:024096 024096 LAIS. [1] ;, mRNA
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TCTGATGCTGCTAAGGCTGAGCATAACATGAATAAAATGTCAACCGAAGATCCTCGACAA
                                                                                                                                                                   GTCAGAAATCCACCCAAATTTGGGACGCATCATAAAGCCTTGCAGGAAATTCGAAACTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Soares_NFL_T_GBC_S1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fatima Bonaldo.
124 g 214 t …
                                                                                                                                                                                                                                                                                                                                                          543 ATGCTTCAAGACTTGCAAGCTGCTGGATTTGATGAG 578
                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            637 bp.
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95.38;
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Unpublished (1997)
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Matches 609; Conserv
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source

FEATURES

Query Match

637

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BASE COUNT

ORIGIN

EST 12-JUN-2000

mRNA sequence.

6) V)

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Brazil
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KEYWORDS
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ORIGIN
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                                                                   REFERENCE
                                                                              AUTHORS
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                                                                                                                                                            TITLE
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                                                                                                                                                         /note="Organ: breast; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (0.5. Letters Patent application No. 196 7.716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
             (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=RC5-BT0744-260
400-031-G07&t3=2000-04-26&t4=1)
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                                                                                                                                                                                                                                                                                                                                             2605 GCCTATTAATTAGAATGGGCATCTTTCCAGAAAGTCTGGCACGATTCTACATAGCAGAAC 2664
                                                                                                                                                                                                                                                                                                                                                                                                 2665 TTACCTGTGCAGTTGAAAGTGTTCATAAAATGGGTTTTATTCATAGAGATATTAAACCTG 2724
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  URL
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Pred. No. 1.3e-131;
0; Mismatches 4;
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                                                                                           1. .578
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT0744"
                                                 High quality sequence start: 12
High quality sequence stop: 467
Location/Qualifiers
                                                                                                                                                                                                                                         stringency conditions.
 This entry can be
                                     Seq primer: puc 18 forward
                                                                                                                                             /dev_stage="Adult
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ilarity 99.3%;
Conservative
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BQ309028 597 bp mRNA linear EST 16-MAY-2002 MR0-BT4508-060701-003-h06 BT4508 Homo sapiens cDNA, mRNA sequence. BQ309028

BQ309028.1 GI:20851571

DEFINITION

rocus

BQ309028

ACCESSION VERSION

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="#974508"
/dev_stage="Adult"
/note="Organ: breast; Vector: pucl8; Site_l: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
/716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR0&t2=MR0-BT4508-060701-003-h06&t3=2001-07-06&t4=1)
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;:
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 597)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R. Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Naclaukuma, A., Bala, C.S., Simpson, D.H. Brustein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                         Shorgun sequencing of the human transcriptome with ORF expressed
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20202663
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Pred. No. 8.5e-130;
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High quality sequence start: 10
High quality sequence stop: 596.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
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99.0%;
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Matches 583; Conservative
                                                                                                                                                                                                                                                                                                                           sequence tags
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Homo sapiens
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855 ACAGATGT 862
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JOURNAL
COMMENT
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/clone="InAGE:3075474"
/clone="InD="NIH_MGC_52"
/clssue_type="lymph"
/cell_type="garminal center B cells"
/cell_line="MGGS"
/lab_host="hHIOB (LTI)"
/note="vector: p7773-755; site_1: Not!; site_2: Eco RI;
/note="vector: p7773-755; site_l: Not!; site_2: Eco RI;
/note="vector: p7773-755; site_1: Not!; site_2: Eco RI;
/note="vector: p7773-755; s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Email: cgapbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
CLONA Library Arrayed by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the II.M.A.G.E. Consortium/LLNL at:
www-bio.llnh.gov/bbrp/image/image.html
Seq primer: Mill Forward.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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               309 TICTICTCGGAGIACTICAGAAGTIAATCCACAAATGCITCAAGACITGCAAAGCTGCTG 368
                                                                                          688 CAGCAGCTGCCAGACCTATTAATGCCAGCATGAAACCAGGGAATGTGCAGCAATCAGTTA 747
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                                                                     GATTTGATGAGGATATGGTTATACAAGCTCTTCAGAAAACTAACAACAGAAGTATAGAAG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 550)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW502306 550 bp mRNA linear UI-HF-BROp-ajs-c-10-0-UI.rl NIH_MGC_52 Homo sapiens IMAGE:3075474 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                              Indels
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Pred. No. 1.6e-128;
0; Mismatches 3;
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/db_xref="taxon:9606"
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AW502306.1 GI:7116847
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99.5%;
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/tissue_type="carcinoma, cell line"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: bladder; vector: pDNR-LIB (Clontech);
/note="Organ: bladder; vector: pDNR-LIB (ggccattatggcc Site_1: Sfil (ggccattatggcc); Stil (agccattatggcc); Double-stranded cDNA was prepared from cell line RNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov plate: LLCM370 row: m column: 10 High quality sequence stop: 583.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                      495 GCAAATGAAACAAATTCTTCTCGGAGTACTTCAGAAGTTAATCCACAAATGCTTCAAGAC 554
                                                                                                                 BE568367 855 bp mRNA linear EST 15-AU
601341939F1 NIH_MGC_53 Homo sapiens CDNA clone IMAGE:3684273
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Tissue Procurement: ATC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                               555 ITGCAAGCTGCTGGATTTGATGAGGATATGGTTATACAAGCTCTTCAGAAAACTAACAAC
                                                                                                                                                                                                                                                                        615 AGAAGTATAGAAGCAGCAATTGAATTCATTAGTAAAATGAGTTACCAAGATCCTCGACGA
                                                                                                                                                                                                                                                                                              675 GAGCAGATGGCTGCAGCAGCTGCCAGACCTATTAATGCCAGCATGAAACCAGGGAATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        735 CAGCAATCAGTTAACCGCAAACAGAGCTGGAAAGGTTCTAAAGAATCCTTAGTTCCTCAG
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CCCAAATTTGGGACGCATCATAAAGCCTTGCAGGAAATTCGAAACTCTCTGCTTCCATTT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelé
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 855)
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Clone distribution: MGC clone distribution information
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Contact: Robert Strausberg, Ph.D.
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/clone_lib="NIH_MGC_53"
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BE568367
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                                                                                                                                                                                                                  .
9
          adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCGGCGGCGCGCATTATGGCC-3' and 3' adaptor where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 673)
     were used in cloning as follows: 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1464
                                                                                                                                                                                                                                                                                                               TGCAGAGTTCTAGCAAATTTAACTTTCCATCAGGGAGACCTGGAATGCAGAATGGTACTG 1284
                                                                                                                                                                                                                                                                                                                                                                             GACAAACTGATTTCATGATACACCAAAATGTTGTCCCTGCTGGCACTGTGAATCGGCAGC 1344
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                                                                                                                                                                                                                                                CTCCTAATCAAGGACAGAGAGGCATTAGTTCTGTTCCTGTTGGCAGACAACCAATCATCA 1224
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                                                                                                                                                                                                                                                              180 CACCACCTCCATATCCTCTGACAGCAGCAGCTAATGGACAAAGCCCTTCTGCTTACAAACAG
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                                                                                                                                                                                 Length 855;
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                 DB 10;
                                                                                                                                                                                                                  16;
                                                                                                                                                                                13.4%; Score 533.4; DB 1(
96.1%; Pred. No. 6.3e-126;
ive 0; Mismatches 16;
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Best Local Similarity
Matches 612; Conserv
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"Hiramoto,K., Hori,F., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
'M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
'D., Shibata,K., Shinagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
NIKEN Mouse ESTS (Arakawa,T., et al. 2001)
On Aug 1, 2000 this sequence version replaced gi:9643478.
Contact: Yoshihide Hayashizaki.M.
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Fax: 81-45-503-9226
Fmail. con-m.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara, Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa Hayashizaki, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
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UKL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci,P., Shibata,Y., Hayatsu,N., and Hayashizaki,Y.
M., Konno,H., Okazaki,Y., Muramätsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length.cDNA libraries for rapid discovery of new
agines. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y. Muramatsu,M., Inoue,Y., Kira,A, and
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Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
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/dev_stage="2 days pregnant adult"
/lab_host="DH10B"
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/db_xref="taxon:10090"
/clone="E330026M13"
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Uppublished (1999)
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ACCESSION VERSION

AUTHORS TITLE JOURNAL

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REFERENCE

DEFINITION

RESULT 13 BI155504 LOCUS

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/note-"organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
blate: LLAMI1093 row: d column: 02
High quality sequence stop: 648.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng
Tissue Procurement: Lothar Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/strain="120,C57BL/6J.FVB/N"
/db.xref="taxon:10090"
/clone="InMAGE:5033425"
/clone=lib="NCI_CGAP_Mam3"
/tissue_Type="tumor, gross tis
/dev_stage="10 months"
/lab_host="DH10B"
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(http://www.jax.org/resources/documents/dnares/). The DNA
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                                                                                                                                                                                                                BG088986 658 bp mRNA linear EST 26-JAN-2001 ut60g11;y1 Soares_mouse_NMGB_bcell Mus musculus cDNA clone IMAGE:3332540 5' similar to TR:095835 095835 LARGE TUMOR SUPPRESSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T 3']; double-stranded cDNA was ligated to Eco RI addptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector Library is normalized; constructed by Bento Soares and
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1 (bases 1 to 658)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares_mouse_NMGB_bcell"
/lab_host="H10B (phage_resistant)"
/note="Organ: germinal B-cell; Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_l: Not I; Site_2: Eco RI; lst strand cDNA was primed with a Not I
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Sciurognathi; Muridae;
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Contact: Robert Strausberg, Ph.D.
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/clone="IMAGE:3332540"
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1M0072J17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longarce, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                                                                                               /clone_lib="Mouse 10kb plasmid UUGC1M library"
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Insert Length: 10000 Std Error:
Plate: 0072. row: J column: 17
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University of Utah Genome Center
University of Utah
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Fax: 801 585 7177
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 [gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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GRPLSGSGIAAFAQAHPSNGQRVNPPPPPPQVRSVTPPPPPRGGTPPPPRGTTPPPPSWE
PSSQTKRYSGNMEYVISRISPVPPGAWQEGYPPPPLTTSPMNPPSQAQRAISSVPVGR
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Brownstein, D.G., Parlow, A.F., McGrath, J. and Xu, T.
Mice deficient of Lats1 develop soft-tissue sarcomas,
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tumor suppressor 1 (Lats1) mRNA,
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/protein_id="AAD16883.1"
/db_xref="G1:4324436"
                                  4 (bases 1 to 3213)
Tao,W. and Xu,T.
Direct Submission
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Congress Ave BCMM 254D, New Haven,
Location/Qualifiers
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suppressor modulates CDC2 activity
Nat. Genet. 21 (2), 177-181 (1999)
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/organism="Mus musculus"
/db_xref="taxon:10090"
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Mammalia; Eutheria; Rodentia;
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SLVGTPNYIAPEVLLRTGYTQLCDWWSVGVILCEMIVGQPPFLAQTPLETQNKVIIWO
TYSLHIPPOPAKLSPEASDLIILIKLCRGPBEDRLGKRGADEIKAHPFFRTIDFSSDLRQQSA
TYSTHTPPTDTSNFPDYDPDKLWSDGSEERNISDTLSGWYRNGKHPEHAFYEFTFRR
FRDDNGYPYNPFRIEXEYIHSQGSEQQSDEDDQHTSSDGNNRDLYYV"
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                                                                                                                          Length 3213;
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1081 C	ō−ō	CCTACCCCTTTTTCTGAGGGTACAGCTTCAAGTGTGCCTGTCATCCCACCTGTTGCTGAA 1140	
1141 G       1141 G	0 <del>-</del> 0	CTCCAAGCTATCAAGGTCCACCACCGCCTTATCCAA 	
1201 T	H — H	CTGTCCCTCCATATGAGTCAGTAAGTAAGCCCTGCAAAGATGAACAGCCTAGCTTACCC 1260 	
1261		aaggaagatgatatgagaagagtgcggacagtggtgactctggggataaagaaaagaa 1320 	
1321 1321		CAGATTACAACTTCACCTATCACTGTTCGGAAAACAAGAAGATGAAGAAGGAAG	
1381		TCTCGGATTCAGAGTTACTCCCCACAGGCCTTTAAGTTCTTCATGGAGCAGCACGTAGAG 1440 	
1441		aacgiccigaagicicaicagagcgicigcaicggaagaagaagcagciagaaaaig 1500 	
1501		AGATGC        AGATGC	
1561		GAGTCTAACTATATTCGTCTTAAAAGGGCTAAAATGGACAAGTCTATGTTTGTAAAGATA 1620 	
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1681		GCTTTGTATGCAACAAAGACTCTTGGAAAGAAAGACGTTCTGCTCCGAAATCAGGTGGCT 1740 	
1741		CATGTGAAAGCGGAGAGGGATATCCTAGCAGAAGCCGACAATGAGTGGGTGG	
1801 1801		TACTACTCTTTCCAGGACAAGGACAACTTGTACTTTGTGATGGACTACATTCCTGGGGGG 1860 	
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1921		atagcagaacttacctgtgcagttgaaagtgttcataaaatgggtttattattcatagagt 1980 	
1981		ATTAAACCTGATAACATTTTGATTGACCGTGATGGCCATATTAAATTGACTGAC	

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1981 ATTAAACCIGATAACATTTIGATIGACCGIGAIGGCCATATTAAATTGACTGACTTIGGC	OY 2041 TIGIGCACTGGCTTCAGAIGGACACATGACTCCAAGTACTACCAGAGTGGGGATCACCA 21	OY 2101 CGGCAAGATGGATTTCAGTAACGAATGGGGGAGATCCTTCCAATTGTCGGTGTGGG 21	Oy 2161 GACAGACTGAAGCCACTGGAGGGGAGAGCTGGTGGCCAGAGCAGAGGATGTCTAGCCGT 22 Db 2161 GACAGACTGAAGCCACTGGAGGGGAGAGCTGCTGGCTGCTGGCAGCACCAGCAGCAGATGTCTAGCCCAT 22	QY       2221       TCTCTGGTTGGGACTCCCAATTATATTGCACCTGAAGTGCTACTGCGAACAGGATATACA       22         D       111111111111111111111111111111111111	OY 2281 CAGCTGTGACTGGTGGAGTGTTATTCTTTGTGAAATGTTGGTGGGACAACCT 23	QY 2341 CCTTTCTTGGCACAAACCCATTAGAAACACAAATGAAGGTTATCATCTGGCAAACTTCT 24	OY 2401 CTACACATCCTCCTCAAGCTAAGCTGAAGCCTGAAGCCTCTGACTCATTATCAAACTG 24	OY 2461 TGTCGAGGACCAGAAGACGCCTCGGCAAGAACGGTGCTGATGAGATAAAGGCTCATCCA 25	Oy 2521 TTTTTAAGACCATCGATTCTCTAGTCATCTCAGACAGCAGTCTGCTTCATACATCCCT 25	Qy     2581     AAAATCACGCATCCAACAGATACATCCAACTTTGGCCCTGTTGATCCTGATAAATTGTGG     26       DD     2581     AAAATCACGCATCCAACAGATACATCCAACTTTCGACCCTGTTGATCCTGATAAATTGTGG     26	OY 2641 AGCGATGGCAGCGAGGAAAAATATCAGTGACACTCTGAGCGGATGGTATAAAAATGGG 27	Oy 2701 AAGCACCCCGAGCACGCTTTCTATGACTTCACCTTTCGGAGGTTTTTGATGACAATGGC 27	Oy 2761 TACCCATATAATTATCCAAAGCCTATTGAGTATGAATACATTCATT	Oy 2821 CAACAGTCTGATGAAGATGATCAACACACAGGTCCGATGGAAACAACCGAGATCTAGTG 28	Oy 2881 TATGTTAATAACTAGGAGATCATTGTAAGAATTTGCAAGAGGCCTGAAGTGCAGGGGT 29  11	OY 2941 TTTCAAGTTTTGAGAAAATTATGCAAATGTGACAGAGTTTGTGTGCTCTGTGTACAATA 30	OY 3001 TTTATTTCCTAAGTTATGGGAAATTGTTTAAAATGTTAATTTATTCACCCTTTTAA 30	Oy 3061 TTCAGTAATTTAGAAAAATTGTTATAAGGAAAGTAAATTATGAACTGAGTATTATAGC 31. 

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B GTGACTCGGCAGCCACCACCATATCCTCTGACCCCAGCTAATGGACAAAGCCCCTCT	B GCTTTACAAACAGGGGCTTCTGCTGCTCCACCATCATTCGCCAATGGAAACGTTCCTCAG 	8 TCGATGATGGTGCCCAACAGGAACAGTCATAACATGGAGCTTTATAATATTAATGTCCCT	8 GGACTGCAAACAGCCTGGCCCCAGTCGTCTGCTCTGCGCAGTCATCCCCAAGCGTT	8 GGGCANGAAATTCCTACATGGCAACCTAACATACCAGTGGGGTCAAATTCTTTTAATAAC 	8 CCATTAGGAAGTAGAGCAAGTCACTCTGCTAATTCTCAGCCTTCTGCCACTACAGTCACT	B GCCATCACCCGCTCCTATTCAACAGCCCGTGAAAAGCATGCGCGTCCTGAAACCAGAG 	8 CTGCAGACTGCTTTAGCCCCAACCCATCCTTGTGTGCCACAGCCAGTTCAGACTGTT	B CAGCCTACCCCTTTTTCTGAGGTACAGCTTCAAGTGTGCCTGTCATCCACTGTTGCT	B GAAGCTCCAAGCTATCAAGGTCCACCACCGCCTTATCCAAAACATCTGCTACACAAAAC	B CCATCHGTCCCTCCATATGAGTCAGTAAGTCAGGCCCTGCAAGATGAACACCCTAGGTTA	B CCCAAGGAAGATGATAGTGAGAAGAGTGGGGACAGTGGTGACTCTGGGGATAAAGAAAAG 	B AAACÄGATTACAACTTCACCTATCACTGTTCGGAAAAACAAGAAGAAGGAGGAGA 	8 GAGTCTCGGATTCAGAGTTACTCCCCACAGGCCTTTAAGTTCTTCATGGAGCAGCAGTA 	B GAGAACGTCCTGAAGTCTCATCAGCAGCGTCTGCATCGGAAGAAGCAGCTAGAAATGAA 	B ATGATGCGGGTTGGATTATCTCAAGATGCCCAGGATCAAATGAGAAAGATGCTTTGCCAG 	8 AAAGAGTCTAACTATATTCGTCTTAAAAGGGCTAAAATGGACAAGTCTATGTTTGTAAAG 	B ATAAAGACATTAGGAATAGGAGCGTTTGGTGAAGTCTGTCT
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	q	<del>, i</del>	sctttgtatgcaacaaaactcttcgaagaagatgttcttcgaaatgag.	
	y g	1738	GCTCATCTGAAAGCGAGAGGGATATCCTAGCAGAAGCCGAAATGAGTGGGTGG	1797 2531
	QY	. 5	IGTACTACTCTTTCCAGGACAAGGACAACTTGTACTTTGTGATGGACTACATTCCTGG	2
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	ΟŊ	1858	GGGATATGATGAGCCTATTAATTAGAATGGGCATCTTTCCTGAAAATCTGGCACGATT	1917
	· Dp	2592	GGTGATATGATGAGCCTATTAATTAGAATGGGCATCTTTCCAGAAAGTCTGGCACGATTC	2651
	Qγ	1918	TACATAGCAGAACTTACCTGTGCAGTTGAAAGTGTTCATAAAATGGGTTTTATTCATAGA	1977
,	qq	2652	ACATAGCAGAACTTACCTGTGCAGTTGAAAGTGTTCATAAAATGGGTTTTATTCATAG	2711
	ΟŊ	- 1	GATATTAAACCIGATAACATTTTGATTGACCGTGATGGCCATATTAAATTGACTGAC	m
	g	2712	attaaaccigataatatitigatigatcgigatggicatattaaatigactgacti	2771
	Oy.	2038	OCTTGTGCACTGGCTTCAGATGGACACATGACTCCAAGTACTACCAGAGTGGGGATCA	
	q <sub>Q</sub>	2772	CTCTGCACTGGCTTCAGATGGACACGATTCTAAGTACTATCAGAGTGGTGA	2831
	Qy	2098	ACGGCAAGATAGCATGGATTTCAGTAACG	2157
	QQ	2832	CACGGCAAGATAGCATGGATTTCAGTAATGAATGGGGGGATCCCTCAAGCTGTCG	2891
	Qy	2158	GGGACAGACTGAAGCCACTGGAGCGGAGAGCTGCTCGCCAGCACCAGGGGT	2217
	g .	2892	ACAGACTGAAGCCATTAGAGCGGAGGCTGCACGCCCAGCACCAGCGATGTCT	2951
	οy	21	CATTCTCTGGTTGGGACTCCCAATTATATTGCACCTGAAGTGCTACTGCGAACAGGATAT	27
	qq	2952	;TTTGGTTGGGACTCCCAATTATATTGCACCTGAAGTGTTGCTACGAACAGG	3011.
	QY .	27	ACACAGCTGTGTGGCTGGTGGAGTGTTGGTTGTTTGTTGGTGAAATGTTGGTGGGCGACAA	33
	qq	3012	CACAGITGIGAGITGGIGGAGIGITGGIGITAIICITITIGAAAIGITGGIGGGA	3071
	δλ		CCTCCTTTCTTGGCACAAACCCC	39
	QQ	3072	crecriterreceacaaacaccarragaaacacaaargaaggrararcaacrege	$\vdash$
1	ōλ	2398	Ö —	2457
	qq		ciciicacairccacacaagciaaacicagiccigaagcircigarcii	3191
	δλ	LCI	CTGTGT	2517
	Dp	3192	CTTTGCCGAGGACCCGAAGATCGCTTAGGCAAGAATGGTGCT	2
	δŏ	2518	CATTT	2577
	QQ	3252	TTTTTAAAACAATTGACTTCTCCAGTGACCTGAGACAGCAGTCTGCTTCATACAT	3311
	ολ	2578	AAAATCACGCATCCAACAGATACA	2637
	qq	3312	CTAAAATCACACCCCAACAGATACATCAAATTTTGATCCTGTTGATCCTGATAAATT	3371
	Qy	2638	CAG	2697
	qq	3372	ggagtgatgataacgaggaagaaatgtaaatgacactctcaatggatgtat	3431
	Οy	2698	TTC	2757
	qq	3432	GAAAGCATCCTGAACATGCATTCTATGAATTTACCTTCCGAAGGTTTTTTGAT	3491
	QY	2758	GGCTACCCATATAATTATCCAAAGCCTATTGAGTATGAATACATTCATT	2817

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Query Match
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John, M.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (04-NOV-1998) Genetics, HHMI, Yale University, 295 Congress Ave BCMM 254D, New Haven, CT 06536, USA
                                                                     3552 GAGCAGCAGTCGGATGAAGATGATCAAAACACAGGCTCAGAGATTAAAAATCGCGATCTA
                                                                                                                2878 GTGTATGTTTAATAAACTAGGAGATCATTGTAA----GAATTTGCAAGAGGCCTGAAGTG
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suppressor modulates CDC2 activity
Nat. Genet. 21 (2), 177-181 (1999)
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Identifying tumor suppressors in genetic mosaics:
lats gene encodes a putative protein kinase
Development 121 (4), 1053-1063 (1995)
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ERRESRIQSYSPQAFKFFMEQHVENVLKSHQQRLHRKKQLENEMMRVGLSQDAQDQMR
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Kishimoto,T., Niwa,S.-i., Nagamine,Y., Nishiyama,Y. and Saya,H.
WARTS protein, polynucleotide encoding the same, antisense
polynucleotide thereof, and antibody recognizing the protein
Patent: Japan (PCT/1998/03739) 24 Aug. 1998;
Sumitomo Electric Industries, Ltd.; I Taya-cho, Sakae-ku,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A human homolog of Drosophila warts tumor suppressor, h-warts, localized to mitotic apparatus and specifically phosphorylated during mitosis
FEBS Lett. 459 (2), 159-165 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (30-JUN-1999) Tumor Genetics and Biology, Kumamoto University School of Medicine, 2-2-1 Honjo, Kumamoto 860-0811,
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Homo sapiens WARTS protein kinase (WARTS) mRNA, complete cds.
AF164041
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Nulshiyama,Y., Hirota,T., Morisaki,T., Hara,T., Marumoto,T.,
Iida,S., Makino,K., Nakamura,H., Koga,H. and Saya,H.
Direct Submission
GAACAACAGTCTGATGAAGATGATCAACACACAAGCTCCGATGGAAACAACCGAGATCTA
                                                                                                                        GTGTATGTTTAATAAACTAGGAGATCATTGTAA----GAATTTGCAAGAGGCCTGAAGTG
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/db_xref="taxon:9606"
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33. 3425
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Nishiyama, Y., Hirota
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GSAAFSSYTNGS IPQSMMVPNRNSHNMELYNISVPGLQTNWPQSSSAPAQSSPSGHE
IPTWQPNIPVRSNSFNNRLGNRASHSANSQPSATTVTAITPAFIQQPWKSMRVLKPEL
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NPSVPPYFESISK PFKEDQPSLPKEDESEKSYENVDSGDKEKQITTSFTTVRKNKNE
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                                                                                         /procein_id="AAD50272.1"
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GISAFVQAHPSNGQRVNPPPPPQVRSVTPPPPPRGQTPPPRGTTPPPPSWEPNSQTKR
YSGNMEYVISRISPVPPGAWQBGXPPPPLNTSPMNPPNQGQRGISSVPVGRQPIIMQS
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VLRNQVAHVKAERDILAEADNEWVVRLYYSFQDKDNLYFVMDYIPGGDMMSLLIRMG
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PQAKLSPEASDLIIKLCRGPEDRLGKNGADEIKAHPFFRTIDFSSDLRQOSASYIPKI
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	1 CAGAATGGTGGTGGTCAGTCTGATTTTATCGTGCACCAAAATGTCCCCACTGGTTCT 	B GTGACTCGGCAGCCACCACCTCCATATCCTCTGACCCCAGCTAATGGACAAAGCCCCTCT	8 GCTTTACAAACAGGGGCTTCTGCTGCTCCACCATCGCTATGGAAACGTTCCTCAG 	co ++	8 GGACTGCAAACGCGCGCCCAGTCGTCTCTGCTCTGCGCGGTCATCCCCAAGCGGT	8 GGGCATGAAATTCCTACATGGCAACCTAACATACCAGTGAGGTCAAATTCTTTTAATAAC 	B CCATTAGGAAGTAGGGAAGTCACTGCTAATTCTCAGCCTTCTGCCACTACAGTCACT	∞ <b>4</b>	8 CTGCAGACTGCTTTAGCCCCAACCCATCCTTCTTGGATGCCAGCAGCCAGTTCAGACTGTT	8 CAGCCTACCCCTTTTTCTGAGGTACAGCTTCAAGTGTGCCTGTCATCCCACCTGTTGCT	B GAAĞTICCAAGCTATCAAGGTCCACCACCGCCTTATCCAAAACATCTGCTACACCAAAAC	8 CCATCTGTCCCTCCATATGAGTCAGTAAGCCCTGCAAGATGAACAGCTAGCT	8 CCCAAGGAAGATGATAGTGAGAAGAGTGCGGACAGTGGTGACTCTGGGGATAAAGAAAG	B AAACAGATTACAACTTCACCTATCACTGTTCGGAAAAACAAGAAAGA	B GAGTCTCGGATTCAGAGTTACTCCCCACAGGCCTTTAAGTTCTTCATGGAGCAGGAGA 	B GAGAACGTCCTGAAGTCTCATCAGCAGCGTCTGCATCGGAAGAAGAGCAGCTAGAAAATGAA	8 ATGATGCGGGTTGGATTATCTCAAGATGCCCAGGATCAAATGAGAAGATGGTTTGCCAG 	B AAAGAGTCTAACTATATTCGTCTTAAAAGGGCTAAAATGGACAAGTCTATGTTTGTAAG 	
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1677 2273 1797 2333 2393 1737 1857 1917 2453 2513 2573 2097 2633 1977 2037 2157 2693 2217 2753 2873 2397 2933 2517 3053 2577 3113 2637 2277 2813 2337 2457 2993 2754 CATTCTTTGGTTGGACTCCCAATTATATTGCACCTGAAGTGTTGCTACGAACAGGATAC 2934 TCTCTTCACATTCCACCACAAGCTAAACTCAGTCCTGAAGCTTCTGATCTTATTATAAA AAAGCTTTGTATGCAACAAAGACTCTTCGAAAGAAAGACGTTCTGCTCCGAAATCAGGTG CIGTACTACTCTTCCAGGACAAGGACAACTTGTACTTGTGATGGACTACATTCCTGGG 2038 GCCTTGTGCACTGCCTTCAGATGGACACATGACTCCAAGTACTACCAGAGTGGGGATCAC 2694 GGAGACAGACTGAAGCCATTAGAGCGGAGAGCTGCACGCAGCAGCAGCGATGTCTAGCA 2874. CCTCCTTCTGGCACAAACACCATTAGAAACACAAATGAAGGTTATCAACTGGCAAACA CTGTGTCGAGGACCAGAAGACCGCCTCGGCAAGAACGGTGCTGATGAGATAAAGGCTCAT 2994 CTTTGCCGAGGACCCGAAGATGGCTTAGGCAAGAATGGTGGTGGAAGATAAAAGGTCAT CCATTTTTTAAGACCATCGATTTCTCTAGTGATCTGAGACAGCAGTCTGCTTCATACATC 2274. GCTCATGTTAAGGCTGAGAGATATCCTGGCTGAAGCTGACATGAATGGGTAGTTGGT GGGGATATGATGAGCCTATTAATTAGAATGGGCATCTTTCCTGAAAATCTGGCACGATTC TACATAGCAGAACTTACCTGTGCAGTTGAAAGTGTTTCATAAAATGGGTTTTATTCATAGA CCACGCCAAGATAGCATGGATTTCAGTAACGAATGGGGAGATCCTTCCAATTGTCGGTGT 2634 CCACGGCAAGATAGCATGGATTTCAGTAATGAATGGGGGGGATCCCTCAAGCTGTCGATGT GGGGACAGACTGAAGCCACTGGAGCGGAGAGCTGCTCGCCAGCACCAGCGATGTCTAGCC CATTCTCTGGGTTGGGACTCCCAATTATATTGCACCTGAAGTGCTACTGCGAACAGGATAT 2278 ACACAGCTGTGTGACTGGTGGAGTGTTGGTGTTATTCTTTGTGAAATGTTGGTGGACAA CCTCCTTTCTTGGCACAAACCCCATTAGAAACACAAAATGAAGGTTATCATCTGGCAAACT TCTCTACACATCCCTCCTCAAGCTAAGCTGAGTCCTGAAGCCTCTGACCTCATATCAAA 3054 CCATTTTTAAAACAATTGACTTCTCCCAGTGACCTGAGACAGCAGTCTGCTTCATACATT TGGAGCGATGGCGAGGAGGAAAATATCAGTGACACTCTGAGCGGATGGTATAAAAAT 2698 GGGAAGCACCCCGAGCACGCTTTCTATGAGTTCACCTTTCGGAGGTTTTTTGATGACAAT 2574 2154 1678 2214 1738 2334 1858 2394 1918 2454 1978 2514 2098 2158 2218 2814 2398 2458 2518 1798 2338 2638 . P ŏ ŏ δŽ qq Dp ŏ q ŏ g ò . q δ g , δy ò Öλ g òγ g ŏ Db ŏ g q g Qγ g g δ

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Toshihiko,K., Shinichiro,T., Kyoko,N., Yasuyuki,N. and Hideyuki,S. Warts Protein, polynucleotide encoding the protein, antisense polynucleotide thereof and antibody recognizing the protein Patent: JP 1999089580-4 1 06-APR-1999;
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PC C12N15/09,C07K14/435,C07K16/18,C12Q1/68,G01N33/53, P
G01N33/532/C12P21/02,
G01N33/532/C12P1/02,C12R1:19),C12N15/00,
PC C12N15/00,PC C12R1:91)
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT Source /organism='Unidentified'.
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DEFINITION

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Direct Submission

Submitted (23-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: Clonerequest@sanger.ac.uk

on Jun 25, 2001 this sequence version replaced gi:14133045.

During sequence assembly data is compared from overlapping clones buring sequences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >- chemistry or covered by high quality data (i.e., phred quality >- chemistry or covered by high quality data (i.e., phred quality >- chemistry or covered by high quality data (i.e., phred quality >- chemistry or covered by high quality data (i.e., phred quality >- chemistry or covered by high quality data (i.e., phred quality >- chemistry or covered by high quality data (i.e., phred quality >- chemistry or covered by high quality data (i.e., phred quality >- chemistry or covered by high quality data (i.e., phred quality >- chemistry or covered by high quality data (i.e., phred quality >- chemistry or covered by high quality data (i.e., phred quality >- chemistry or covered by high quality as confirmed by restriction digest. The following assembly was confirmed by restriction digest. The following aboreviations are used to associate primary accession numbers given the feature table with their source databases: Em:, EMBL: Sw:, SWISSPROT; Tr:, TREMBL: Wp., MORMPEP; Information on the WORMPEP; http://www.sancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.ancer.
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/note="AluJo/FRAM repeat: matches 202. .287 of consensus" 29818. .30056 /note="Rinkar" repeat: matches 1. .105 of consensus" 16076. .16112
//note="Alu repeat: matches 79. .160 of consensus" 16122. .17029
//note="Linkaka repeat: matches 5319. .6300 of consensus" 17080. .17261
//note="MER74A repeat: matches 1. .171 of consensus" //note="MER74A repeat: matches 1. .770 of consensus" //note="Alu87 repeat: matches 1. .296 of consensus" //note="Alu88 repeat // Note="MIR repeat: matches 41. 241 of consensus" 1925. ..19557 // Note="MIR repeat: matches 11. 306 of consensus" 19558. ..19843 // Note="AluSa repeat: matches 12. 294 of consensus" 19558. ..19843 // Note="AluSa repeat: matches 12. 294 of consensus" 20911. .21270 // Note="AluSa repeat: matches 11. 300 of consensus" 21302. ..21313 // Note="FRAM/FAM repeat: matches 4. .72 of consensus" 22015. ..22173 // Note="MRRSB repeat: matches 7. .176 of consensus" 22419. ..231403 matches 2353. .2196 of conseques" /note="AluSg/x repeat: matches 89. 310 of consensus" 24355. 24495 /note="FLAM\_C repeat: matches 2. .125 of consensus" 24659. .24859 /note="MER3 repeat: matches 2. .209 of consensus" 25072. .25249 /note="AluSc repeat: matches 118. .290 of consensus" 25256. .25572 note="MER5A repeat: matches 108. .185 of consensus" /note="Alur repeat: matches 1. .298 of consensus" 18502. .1851 /note="25 copies 2 mer ta 100% conserved" 18552. .18818 /note="Alusp repeat: matches 34. .303 of consensual 18929. .19117 // note="Alusx repeat: matches 1, .309 of consensus" 25575. .25874 note="AluSx repeat: matches 1. .299 of consensus" /note="AluSg repeat; matches 1. .293 of consensus<sup>\*</sup> 30267. .30570 note="AluSq repeat: matches 1. .302 of consensus" 10581. .30762 note="AluJb repeat: matches 1. .312 of consensus" 31127. .31259 .305 of consensus /note=".cpg island" /evidence=not\_experimental /evidence=not\_experimental /evide="44 copies 2 mer cc 64% conserved" 23378. .23453 29260. .29548 /note="Alusg repeat: matches 1. 29567. .29652 30827. .31119

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pred. No. 2.2e-271;
0; Mismatches 212;
      31453. .31645

/note="LlM1 repeat: matches 1407.

32228. .32673

/note="MLTI repeat: matches 100.

32688...32820

/note="FLAM_C repeat: matches 1.
                                                                                                                                                36.4%;
85.9%;
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Best Local Similarity
Matches 1309; Conserv
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Toshihiko, K., Shinichiro, T., Kyoko, N., Yasuyuki, N. and Hideyuk warts Protein, polynucleotide encoding the protein, antisense polynucleotide thereof and antibody recognizing the protein Patent: JP 1999089580-A 2 06-APR-1999;
SUMITOMO ELECTRIC IND LTD
SUMITOMO ELECTRIC ON LTD
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                        56366 GCAATTACACCAGCTCCTATTCAACAGCCTGTGAAAAGTATGCGTGTATTAAAACCAGAG
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GCCATCACACCCGCTCCTATTCAACAGCCCGTGAAAAGCATGCGCGTCCTGAAACCAGAG
                                                                           CTGCAGACTGCTTTAGCCCCCAACCCATCCTTGGATGCCACAGCCAGTTCAGACTGTT
                                                                                               CAGCCTACCCCTTTTTCTGAGGGTACAGCTTCAAGTGTGCCTGTCATCCCACCTGTTGCT
                                                                                                                                                                        TOSHIHIKO KISHIMOTO, SHINICHIRO TAMBA, KYOKO NAGAMINE,
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PC CI2N15/09,00144/435,C07K16/18,C12Q1/68,G01N33/53, F
G01N33/532/7(212P21/02,
PC (C12N15/09,C12R1:91),(C12P21/02,C12R1:19),C12N15/00,
(C12N15/00, PC C12R1:91)
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CC Strandedness: Double,
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unidentified.
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                                                                                                     Score 1126.8; DB 6; Length
Pred. No. 2.6e-261;
0; Mismatches 147; Indels
                     l. .1374
⁄organism='Unidentified'
            location/Qualifiers
                                                                            392
                                                       /organism="unidentified"
/db_xref="taxon:32644"
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  Linear;
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89.2%;
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Matches 1226; Conserv
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Mus musculus clone RP24-258P4, WORKING DRAFT SEQUENCE, 17 unordered
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Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                              CAAGCTAAACTCAGTCCTGAAGCTTCTGATCTTATTATTAAACTTTGCCGAGGACCCGAA
                                                                                         TGGAGTGTTGGTGTTATTCTTTGTGAAATGTTGGTGGGACAACCTCCTTTCTTGGCACAA
                                                                                                                                                ACCCCATTAGAAACACAAATGAAGGTTATCATCTGGCAAACTTCTCTACACATCCCTCCT
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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Mammalia; Eutheria; Rodentia;
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contig of 18800 bp in length 51: gap of 100 bp 85997: contig of 15046 bp in length 75: gap of 100 bp 70851: contig of 12976 bp in length

104897: com

86097 70951

p of 100 bp contig of 9046 bp in length

1162: gap of 100 bp 48629: contig of 3467 b 729: gap of 100 bp 577.75: contig of 9046 h

48729:

57875:

bp in length

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04898 104997
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Matches 1091;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (21.40G-2002) Whitehead Institute/MIT Center for Genome Research, 320 charles Street, Cambridge, MA 02141, USA On Aug 21, 2002 this sequence Version replaced gi:17060822. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                       Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A.;
Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad Toh, K.,
Lui, G., MacClean, C., Macdonald, P., Major, J., Matthews, C.,
McCarthy, M., Meldrim, J., Menous, L., Mihova, T., Mienga, Y.,
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H.,
O'Connor, T., O'Donnell, P., O'Nell, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P.,
Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 164490)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vasslliev,H.,
Viel,R., Vo.A., Wilson,B., Wu.X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
                                                                                                                                  Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastlen, Y., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                    Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the gaps are unknown the finished sequence
                                                                                                                                                                                                                                         Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality coverage: 7.2 in Q20 bases; agarose-fp quality coverage: 7.8 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \verb|http://ftp.genome.washington.edu/RM/RepeatMasker.html|\\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: Plasmid; n/a: 100% of reads Chemistry: Dye-terminator Big Dye: 100% of read
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .00 bp
f 1085 bp in length
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f 3274 bp in Length.
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1268 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0: gap of 100 bp
11116: contig of 2926 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: Phrap; version 0.960731 Consensus quality: 158929 bases at least 040 Consensus quality: 161241 bases at least 030 Consensus quality: 162174 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1303: contig of 1303 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 bp
of 760 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert size: 176000; agarose fp
Insert size: 162890; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the exact sizes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  name: L19333
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.: gap of

3531: cr

? 3631: cr
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1404 2163: co
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Center clone name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     code: WIBR
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JOURNAL
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                                                                                                                    REFERENCE
AUTHORS
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COMMENT

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61 CAGAGACACGCCCCATCTCTAGGAGAAATGTGGTTTATCGTTCTGAAAGCCCCAACTCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GTGCAACATTCAATTAACCGAAAACAAAAGCTGGAAAGGTTCTAAAAGAGTCTCTAGTTCCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 164490;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
120197: gap of 100 bp
120197: contig of 15200 bp in length
0297: gap of 100 bp
136805: contig of 16508 bp in length
                                                                          5005: gap of 100 bp
160104: contig of 23199 bp in length
1204: gap of 100 bp
                                                                                                                            contig of 4286 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.6%; Score 1079.4; DB 2; 99.8%; Pred. No. 9.6e-250;
                                                                                                                                                                                                                                     clone_lib="RPCI-24 Male Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vector_side:right"
47330 a 35286 c 34742 g 45505 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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note="assembly_fragment"
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ote="assembly_fragment"
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note="assembly_fragment"
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                                                                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP24-258P4"
                                                                                                                                                   Location/Qualifiers
                                                                                               ..... gap of
164490: cor'
tion'
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                                                                              36806"136905
                                           20198 120297
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AC	POURS ACTERNITION MUSTER NOTE TO THE PROPERTY OF THE PROPERTY																	
LOCUS	ACCESSION VERSION	KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE	JOURNAL REFERENCE AUTHORS			·			TITLE JOURNAL REFERENCE	AUTHORS				•			
			,		· · · · · ·													
5853 CAGAGACACGCCCATCTCTAGGAGAAAATGTGGTTTATCGTTCTGAAAGCCCCAACTCA 5794	121 CAGGCGGATGTAGGAAGACCTCTGTCTGGATCCGGCATTGCAGCATTTGCTCAGGTCAC 180 [	181 CCAAGCAATGGACAGAGAGTGAACCCCCACCACCACCTCAAGTTAGGAGTGTTACTCCT 240	241 CCACCACCTCCGAGAGGCCAGACCTCCCGGAGGCACCACTCCCCCTCCCCCTCA 300	301 TGGGAACCAAGCTCTCAGACAGAAGCGCTACTCTGGGAACATGGAGTACGTAATCTCCCGA 360 	361 ATCTCCCCTGTTCCACCTGGGGGGTGGCAGAGGGGTACCCTCCACCACTCTTACCACT 420	421 TCTCCCATGAATCCCCTAGCCAGGCTCAGAGGCCCATTAGTTCTGTTCCAGTTGGTAGA 480	481 CAACCCATCATCATGAGGAGTACTAGCAAATTTAACTTTACACCAGGGGACCTGGAGTT 540	541 CAGAATGGTGGTGGTCAGTTTTATCGTGCACCAAAATGTCCCCACTGGTTCTGTG 600	601 ACTCGGCACCACCACCTCCATATCCTCTGACCCCAGCTAATGGACAAAGCCCCTCTGCT 660 [	661 TTACAAACAGGGGCTTCTGCTGCTCCACCATTCGCCAATGGAAACGTTCCTCAGTG 720 	721 ATGATGGTGCCCAACAGGAACAGTCATAACATGGAGCTTTATAATATTAATGTCCCTGGA 780	781 CIGCAAACAGCCIGGCCCCAGICGICTICIGCICCIGCGCAGICAICCCCAAGCGGIGGG 840	841 CATGAAATICCTACATGGCAACCTAACATACCAGTGAGGTCAAATTCTTTTAATAACCCA 900 	901 TTAGGAAGTAGAGCAAGTCACTCTGCTAATTCTCAGCCTTCTGCCACTACAGTCACTGCC 960	961 ATCACACCGGTCCTATTCAACAGCCGTGAAAAGCATGGGGGGTCCTGAAACCAGAGCTG 1020 	1021 CAGACTGCTTTAGCCCCAACCCATCCTTCTTGGATGCCACAGCCAGTTCAGACTGTTCAG 1080	1081 CCTACCCCTTTT 1093 	
qq	Oy Dp	Qy Dp	Qy	Oy Dp	Oy Dp	Qy Db	Qy Db	Oy Dp	Qy Dp	Qy Dp	Qy Dp	Qy Dp	Oy Dp	oy Ob	Oy Dp	Qy Db	Oy Dp	

RESULT 10 AC102712

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Birren, B.

Birren, B., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barren, N., Bastien, Y., Bloom, T., Boguslavkiy, L., Boukhqalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., Deratlano, K., Dewar, K., Dalaz, J.S., Dodge, S., Farco, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Farco, S., Grahan, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Macdonald, P., Major, J., Matthews, C., MacLean, C., Macdonald, P., Major, J., Matthews, C., MacLean, C., Madonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Norbu, C., Nicol, R., Norbu, C., Norman, C., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Kise, C., Rogov, P., Smith, C., Spencer, B., Stange-Thoman, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vasslilev, H., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Dirert, S., Mineir, C., Zamer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Upublished

(bases 1 to 164490)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Boguslavkky, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Changaro, Chazaro, B., Cohoepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cook, P., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galgan, J., Gardyna, S., Gords, S., Goyette, M., Graham, L., Gardyna, S., Gords, S., Goyette, M., Graham, L., Grand-Pierre, N., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Landers, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., Macdonald, P., McKernan, R., Mebheeters, R., Liu, G., Macher, J., McKernan, R., Mebheeters, R., Neular, J., Neular, J., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., O'Liver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Santos, R., Schauer, S., Schupback, R., Rieback, M., Spencer, B., Staganon, J., Rosettl, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Pierre, M., Spencer, B., Staganon, J., Phondore, J., Royer, J., Spencer, B., Staganon, S., Severy, P., Spencer, B., Staganon, S., Severy, P., Spencer, B., Staganon, J., Phondore, J., Royer, J., Phondore, J., Phondore,
02712 164490 bp DNA linear HTG 21-AUG-2002 musculus clone RP24-258P4, WORKING DRAFT SEQUENCE, 17 unordered
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11 repeats were identified using RepeatMasker:

mit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker.html
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IG; HTGS_PHASE1; HTGS_BRAFT; HTGS_FULLTOP.
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DD 137509 ACCCCTTATCCAAAACATCTGCTACCAAAACNCCATCTGTCCCTCCATATGAGTCAG 137568
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                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                    Quality coverage: 7.2 in Q20 bases; agarose-fp Quality coverage: 7.8 in Q20 bases; sum-of-contigs
                        Center clone name: 258_P_4
Sequencing vector: Plasmid; n/a; 100% of reads
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0:960731
Consensus quality; 158929 bases at least 030
Consensus quality; 161241 bases at least 030
Consensus quality; 161241 bases at least 020
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1268 bp in length .
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164490: contig of 4286 bp in length
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f 1085 bp in length
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f 3274 bp in length
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contig of 2926 bp in length
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Insert size: 162890; sum-of-contigs
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41036: contig of 29
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1; Gaps

Indels

Score 872.4; DB 2; Pred. No. 1.1e-199; 0; Mismatches 1;

Length 164490;

1627 others

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GTGCGGACACTGTGACTCTGGGGATAAAGAAAAGAAACAGATTACAACTTCACCTATCA 1342 	CTGTTCGGAAAACAAGAAGATGAAGAACGAAGAGTCTCGGATTCAGAGTTACTCC 1402 	CACAGGCCTTTAAGTTCTTCATGGAGCAGCACGTAGAGAACGTCCTGAAGTCTCATCAGC 1462 	AGCGTCTG ATCGGAAGAAGCAGCTAGAAATGAAATGATGCGGGT 1508 	£	457.1 GI:20252345 "n. "n.	d. to 3155) to 3155) W., Wang, W., Zha sequences of lat 6359193-A 7 19-M cation/Qualifier 3155	/organism="unknown" 51 a 924 c 894 g 586 t	Similarity 65.1%; Score 812.6; DB 6; Length 3155; 7; Conservative 0; Mismatches 644; Indels 18; Gaps	CACTCTGCTAATTCTCAGCCTTCTGCCACTACAGTCACTGCCATCACCCGCTCCTATT 978	CAACAGCCCGTGAAAAGCATGCGCGTCCTGAAACCAGAGCTGCAACTGCTTTAGCCCCA 1038	ACCCATCCTTCTTGGATGCCACAGCCAGTTCAGACTGTTCAGCCTACCCCTTTTTCTGAG 1098	GGTACAGCTTCAAGTGTGCCTGTCATCCCACCTGTTGCTGAAGCTCCAAGCTATCAAGT 1158	CCACCACCGCCTTATCCAAAACATCTGCTACACAAAACCCATCTGTCCCTCCATATGAG 1218 	TCAGTAAGTAAGCCTGCAAAGATGAACAGCCTAGCTTACCCAAGGAAGATGATAGTGAG 1278	AAGAGTGGGGACAGT	ATTACAACTTCACCTATCACTGTTCGGAAAAACAAGAAAGA
GTGCGGA           GTGCGGA	CTGTTCG              CTGTTCG	CACAGGC 	AGCGTCT 			O	, ,	h Simi 37;	CACTCTG	CAACAGO	ACCCATC         TCGCACC	GGTACAGO   GAGGGCA	CCACCACI 	TCAGTAA	AAGAGTG	ATTACAA        ATTCAGA
1283 137629	1343 137689	1403 137749	1463 137809	RESULT 11 AR201457 LOCUS DEFINITION ACCESSION	VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL FEATURES	BASE COUNT ORIGIN	Query Matcl Best Local Matches 12	919	979	1039	1099	1159	1219	1279	1324
Qy	Oy Dp	δ δ	Qy Db	RESUL AR201 · LOCUS DEFIN ACCES	KEY SOU	REFI AI TI JC FEAS	BASI	ōmx	· Qy	S S	δ da	oy Ob	Q Q	Oy Dp	<sup>2</sup> ලි	. <sup>6</sup>

1863 1923 2043 2103 2163 2463 1524 1563 1683 1743 1824 2064 2124 2184 2244 . 2223 2304 2343 2544 1644 GCAGAACTTACCTGTGCAGTTGAAAGTGTTCATAAAATGGGTTTTATTCATAGAGATATT 1983 2283 2484 1384 CGGATTCAGAGTTACTCCCCACAGGCCTTTAAGTTCTTCATGGAGCAGCACGTAGAGAAC 1443 1584 TCTAACTATATTCGTCTTAAAAGGGCTAAAATGGACAAGTCTATGTTTGTAAAGATAAAG 1623 2365 CTCTGTGACTGGTGGAGGTCGGTGGATTCTCTTTGAGATGCTGGTTGGCAGCGCCCT 2424 TTCTTGGCACAAACCCCATTAGAAACACAAATGAAGGTTATCATCTGGCAAACTTCTCTA 2403 1465 CGCATCAAGAGTTACTCCCCTTATGCCTTCAAATTCTTCATGGAGCAACACGTGGAGAAT AAACCTGATAACATTTTGATTGACCGTGATGGCCATATTAAATTGACTTTTGGCTTG 1504 CGGGTTGGATTATCTCAAGATGCCCAGGATCAAATGAGAAAGATGCTTTGCCAGAAAGAG ACATTAGGAATAGGAGCGTTTGGTGAAGTCTGTCTAGCAAGAAAAGTCGATACTAAAGCT. TTGTATGCAACAAAAAACTCTTCGAAAGAAGACGTTCTGCTCCGAAATCAGGTGGCTCAT 1765 CTGTACGCCATGAAGACTCTCAGGAAGAAGGATGTCCTGAACCGGAATCAAGTGGCCCAT TACTCTTTCCAGGACAAGGACAACTTGTACTTTGTGATGGACTACATTCCTGGGGGGGAT ATGATGAGCCTATTAATTAGAATGGGCATCTTTCCTGAAAATCTGGCACGATTCTACATA CAAGATAGCATGGATTTCAGTAACGAATGGGGAGATCCTTCCAATTGTCGGTGTGGGGAC AGACTGAAGCCACTGGAGCGGAGAGCTGCTCGCCAGCACCAGCGATGTCTAGCCCATTCT CTGGTTGGGACTCCCAATTATATTGCACCTGAAGTGCTACTGCGAACAGGATATACACAG CTGTGTGACTGGTGGAGTGTTGGTGATTGTTGAAATGTTGGTGGGACAACCTCCT 1525 1645 1705 1924 1984 2185 2305 1444 1585 1564 1624 1744 1825 1864 2005 2065 2104 2245 2284 2344 2425 1684 1804 2164 ò d δ g ŏ q ó Op QΥ q Qγ d Q q g ŏ g δλ ζ δ g Óγ d δ g δλ Dβ Dp Ω δ q δλ δ ò δ

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KAQGGPPASLTFPAHAGLYTASHHKPAATPPGAHPLHVLGTRGPTFTGESSAQAVLAP
SRNSLNADLYELGSTVPWSAAPLARRDSLQKQGLEASRPHVAFRAGFSRTNSFNNPQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus MmLATS2 mRNA for warts/lats-like kinase, complete cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                         2703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (sites)
Yabuta, N., Fujil, T., Copeland, N.G., Gilbert, D.J., Jenkins, N.A., Nishiguchi, H., Endo, Y., Toji, S., Tanaka, H., Nishimune, Y. and
                                                                                                                                                                                                                                                                                                                                          2782 CATCCAGAGCACGCCTTCTATGAGTTCACCTTCCGCAGGTTCTTCGATGACAACGCCTAT 2841
                                                                                                                                                                                                                                                                               2725 GAGGCCAGCGGAGAG ---AGCGCCAAGGCCTGGGACACGCTGGCCTCCCCCAGCAGCAAG 2781
                                                                                                                                                                                                                                                                                                                       CACCCCGAGCACGCTTTCTATGAGTTCACCTTTCGGAGGTTTTTTGATGACAATGGCTAC 2763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (22-FEB-1999) Hiroshi Nojima, Research Institute for
Microbial Diseases, Osaka University, Department of Molecular
Genetics; Yamadacka 3-1, Suita, Osaka 565-0871, Japan
(E-mail:hnojima@biken.osaka-u.ac.jp, Tel:81-6-6875-3980,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         homologue of the Drosophila tumor suppressor gene lats/warts
Genomics 63 (2), 263-270 (2000)
                                                                                                2605 TICAACATCGACTTTTCCCGTGACATCCGAAAGCAGGTGCACCCTACGTCCCACC
2464 CGAGGACCAGAAGACCGCCTCGGCAAGAACGGTGGTGATGAGATAAAGGCTCATCCATTT
                                                                           TTTAAGACCATCGATTTCTCTAGTGATCTGAGACAGCAGTCTGCTTCATACATCCCTAAA
                                                                                                                                                         ATCACGCATCCAACAGATACATCCAATTTCGACCCTGTTGATCCTGATAAATTGTGGAGC
                                                                                                                                                                                                                                         GATGGCAGCGAGGAGAAATATCAGTGACACTCTGAGCGGATGGTATAAAAATGGGAAG
                                   2545 TGCGCGGCTGACTGCCGCCTGGGCAGGGATGGGGCAGATGACCTCAAGGCACACCCGTTC
                                                                                                                                                                                                 2665 ATCAGCCACCCCATGGACACCTCCAATTTTGACCCGGTGGATGAAGAAAGCCCCTGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                     2764 CCATATAATTATCCAAAGCCTATTGAGTATGAATACATT 2802
                                                                                                                                                                                                                                                                                                                                                                                                                                             2842 CCCTTCCGGTGCCCGAAGCCCTCAGAGCCCGCAGAGAGT 2880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="warts/lats-like kinase"
/protein_id="BAA92380.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="GI:7212786
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1. .3460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus cDNA to mRNA.
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Nojima, H. and Fujii, T.
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HVENVIKTYQQKVSRRLQLEQEVAKAGLCEAEQEQMRKILYQKESNYNRLKRAKMDKS
MFVKIKTLGIGAFGEVCLACKLDTHALYAMKTLRKKDVLNRNQVAHVKABRDILAEAD
                                                                                                                                                                                                          LWDDVSNCRCGDRLKTLEGRAGKGHQRCLAHSLVGTPNYIAPEVLLRKGYTQLCDWWS
VGVILPEMLVGQPPFLAPTPTETQLKVINWESTLHIPTQVRLSAEARDLITKLCCAAD
                                                                                                                                                                                    HKMGFIHRDIKPDNILIDLDGHIKLTDFGLCTGFRWTHNSKYYQKGNHMRQDSMEPGD
                                                                                                                                                                                                                                                                       CRLGRDGADDLKAHPFFNTIDFSRDIRKQPAPYVPTISHPMDTSNFDPVDESPWHEA
SGESAKAWDTLASPSSKHPEHAFYEFTFRRFFDDNGYPPRCPKPSEPAESADPGDADL
EPSLPAPNTVTAVTAAHILHPVKSVRVLRPEPQTAVGPSHPAWVAAPTAPATESLETK
                               EGSAGPHPLDVDYGGSERRCPPPPYPKHLLLPSKSEQYSVDLDSLCTSVQQSLRGGTE
                                                            QDRSDKSHKGAKGDKAGRDKKQ1QTSPVPVRKNSRDEEKRESR1KSYSPYAFKFFMEQ
                                                                                                                                                    NEWVVKLYYSFQDKDSLYFVMDYIPGGDMMSLLIRMEVFPEHLARFYIAELTLAIESV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1484 GAGGGCAGGCCCACACACCCGCTGGATGTGGACTATGGCGGCTCCGAGCGCAGGTGC
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Pred. No. 8:8e-184;
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E38226.1 GI:18626935
JP 2000210086-A/1.
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PAT 31-JAN-2002
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Catarrhini; Hominidae; Homo.
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C12N15/09,A61K31/00,A61K38/27,C07K14/47,C07K14/525,C12Q1/6
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Organism='Homo sapiens (human)'.
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Score 787.2; DB 6;
Pred. No. 3.5e-179;
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Koga,J., Kono,K. and N.Z.F.
Human tumor regulatory gene
Patent: JP 2000210086-A 1 02-AUG-2000;
NIHON CHEMICAL RESEARCH K K
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PC A61K37/36, (C12N15/00, C12R1:91)
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PAT 31-JAN-2002
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1 (Dases 1 to 5486)
Koga,J., Kono,K. and N.2.F.
Human tumor regulatory gene
Patent: JP 2000110086-A 2 02-AUG-2000;
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C12N15/09,A61K31/00,A61K38/27,C07K14/47,C07K14/525,C12Q1/68,
2720 TCTATGAGTTCACCTTTCGGAGGTTTTTTGATGACAATGGCTACCCATATAATTATCCAA
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C12R1:91),C12N15/00,
PC A61K37/36,(C12N15/00,C12R1:91)
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E38227
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JP 2000210086-A/2
02-AUG-2000
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JP 2000210086-A/2.
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Best Local Similarity 68.7%;
Matches 1099; Conservative
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Homo sapiens
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                        2419 CCTTTGGAGAAGTGTGCCTTGCTTGTAAGGTGGACACTCACGCCCTGTACGCCATGAAGA
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ocructure, expression, and chromosome mapping of LATS2, a mammalian homologue of the Drosophila tumor suppressor gene lats/warts cenomics 63 (2), 263-270 (2000)
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Homo sapiens HsLATS2 mRNA for large tumor suppressor 2, partial
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Yabuta,N., Fujii,T., Copeland,N.G., Gilbert,D.J., Jenkins,N.A.,
Nishiguchi,H., Endo,Y., Toji,S., Tanaka,H., Nishimune,Y. and
Nojima,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (27-MAY-1999) Hiroshi Nojima, Research Institute for Microbial Diseases, Osaka University, Department of Molecular Genetics; Yamadaoka 3-1, Suita, Osaka 565-0871, Japan (E-mail:hhojima@biken.osaka-u.ac.jp, Tel:81-6-6875-3980, Pax:81-6-6875-5192)
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Nojima, H. and Nishiguchi, H.
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large tumor suppressor 2;
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Human warts gene f
Human large tumour
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Human Lats (large
Human WART1 CDNA.
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17655.667 Million cell updates/sec
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                                                                                                                                                                                                                               1 gtgcaacattcaattaaccg......scccaaaaaaaaaaaaaaaa 3213
                                                                                                                         ; Search time 409.821 Seconds
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/SIDS2/gcgdata/geneseq/genesegn-embl/NA2001B.DAT:*
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                                                                                                                                                                                                                                                                                                                                                          4370478
              GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                   2185239 seqs, 1125999159 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                   nucleic search, using sw model
                                                                                                                     January 16, 2003, 09:50:07
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AAT42118
AAZ51505
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99WO-US19068

18-AUG-1999;

M-lats2 gene encod

3213 3209.8 2483 2481.4 1946.8 1126.8 1012

Score

Result Š. a

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Use of lats proteins, complexes of lats and cdc2 for treating cancer that is refractory to treatment by standard chemotherapy and radiation therapy, and disorders associated with aberrant levels of cdc2 activity
                                 Zhang
                                  RK,
                                   Fukumoto
                                  ×
                                   Fei
980S-0096996
                                  St John MAR,
Stewart RA;
                                                       WPI; 2000-246496/21
                   (UYYA ) UNIV YALE.
                                                              P-PSDB; AAY70391
                                 Xu T, Tao W,
Turenchalk GS,
18-AUG-1998;
18-AUG-1998;
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The present sequence is a DNA encoding mouse Lats (large tumour suppressor) protein which is a cell overprollferation inhibitor and a negative regulator of cell cycle-dependent kinase cdc2/cyclin A.

The present sequence is useful for treating cancer that is refractory to standard chemotherapy or radiation therapy such as hyperplasia, metaplasia, or dysplasia, and disorders associated with aberrant levels of cdc2 activity. Conditions treated by promoting cdc2 function include degenerative disorders, growth deficiencies, hypoproliferative disorders, physical trauma, lesions, and wounds. An animal model prefarably a mouse, in which a lats gene has been disrupted by homologous recombination, e.g. a lats knock-out mouse, is used for screening compounds that can be used to treat or prevent cancer, particularly skin cancer, soft tissue sarcomas and ovarian tumours, and disorders shopponadotropic hypogonadism. The lats DNA is also used in gene therapy. 44; Fig 13; 134pp; English. Claim

Sequence 3213 BP; 946 A; 764 C; 696 G; 807 T; 0 other;

CAGGCGGATGTAGGAAGACCTCTGTCTGGATCCGGCATTGCAGGATTTGCTCAAGCTCAC 180 240 420 9 CAGGCGGATGTAGGAAGACCTCTGTCTGGATCCGGCATTGCCAGCATTTGCTCAAGCTCAC CCACCACCTCCGAGAGGCCAGACCCCACCTCCCCGAGGCACCACTCCCCCTCCCCTCA CACCACCACCAGAGGCCAGACCCCACCTCCCCGAGGCACCACTCCCCCTCCCCTCA TGGGAACCAAGCTCTCAGACAAAGCGCTACTCTGGGAACATGGAGTACGTAATCTCCCGA TCTCCCATGAATCCCCCTAGCCAGGCTCAGAGGGCCATTAGTTCTGTTCCAGTTGGTAGA CCAAGCAATGGACAGAGAGTGAACCCCCCACCACCACCTCAAGTTAGGAGTGTTACTCCT GTGCAACATTCAATTAACCGAAAACAAAGCTGGAAAGGTTCTAAAGAGTCTCTAGTTCCT DB 21; Length 3213; Indels ; 0 Ouery Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3213; Conservative 0; Mismatches Query Match 61 61 121 181 241 301 361 361 421 181 241 301 121 g QQ ò qq g ò QQ ò q ò ö 8 ö g ŏ ò

CAACCCATCATCATGCAGAGTACTAGCAAATTTAACTTTACACCAGGGCGACCTGGGAGTT

481

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1380 1380 1441 AACGTCCTGAAGTCTCATCAGCAGCGTCTGCATCGGAAGAAGCAGCTAGAAATGAAATG 1500 1620 1200 ATGATGGTGCCCAACAGGAACAGTCATAACATGGAGCTTTATAATATTAATGTCCCTGGA 780 CIGCAAACAGCCIGGCCCCAGICGICTTCIGCTCCIGCGCAGICAICCCCAAGCGGTGGG 840 ACTOGGCAGCCACCACCTCCATATCCTCTGACCCCAGCTAATGGACAAAGCCCCTCTGCT 660 GAGTCTAACTATATTCGTCTTAAAAGGGCTAAAATGGACAAGTCTATGTTGTAAAGATA CAGACTGCTTTAGCCCCAACCCATCTTCTTGGATGCCACAGCCAGTTCAGACTGTTCAG GCTCCAAGCTATCAAGGTCCACCACCGCCTTATCCAAAACATCTGCTACAAAACCAAAACCA TCTCGGATTCAGAGTTACTCCCCACAGGCCTTTAAGTTCTTCATGGAGCAGCACGTAGAG CATGAAATTCCTACATGGCAACCTAACATACCAGTGAGGTCAAATTCTTTTAATAACCCA CCTACCCCTTTTTCTGAGGGTACAGCTTCAAGTGTGCCCTGTCATCCCACCTGTTGCTGAA 1501, ATGCGGGTTGGATTATCTCAAGATGCCCAGGATCAAATGAGAAAGATGCTTTGCCAGAAA TTAGGAAGTAGAGCAAGTCACTCTGCTAATTCTCAGCCTTCTGCCACTACAGTCACTGCC ATCACACCCGCTCCTATTCAACAGCCCGTGAAAAGCATGCGCGTCCTGAAAACCAGAGCTG GCTCCAAGCTATCAAGGTCCACCACCGCCTTATCCAAAACATCTGCTACACCCAAAACCA TCTGTCCCTCCATATGAGTCAGTAAGTAAGCCCTGCAAAGATGAACAGCCTAGCTTACCC CAGAATGGTGGTGGTCTGATTTTATCGTGCACCAAAATGTCCCCACTGGTTCTGTG TTACAAACAGGGGCTTCTGCTGCTCCACCATCATTCGCCAATGGAAACGTTCCTCAGTCG 1261 1321 1561 781 901 961 1081 1081 1141 1141 1201 1201 1261 1321 1021 1381 841 196 1021 541 601 661 481 541 661 721 721 781 g g Óλ a ò g ŏ g ŏ Qy Сp ŏ g δy g q ŏ ò 쇰 g

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	2701	2761 TACCCAT 	2821	Qy 2881 TATGTTTAATAAA 	2941	3001	3061	3121	QY 3181 ATANTTTAAAAT	RESULT 2 AAT42119 ID AAT42119 standard,			KW protein-serine/thr KW dominant-negative; KW growth deficiency; KW transgenic plant;	Mus musculus.	CDS	0402-AI. T-1996.	27 -MAR-1995; 9	PA (UXYA) UNIV YALE. XX PI Tao W, Wang W,
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CST AMADA WARDANDA DA WARDA A WARDA WARA WARDANDA WARDA WARD	AAGACATTAGGAATAGGAGCGTTTGGTGAAGTCTGTCTAGCAAGAAAGTCGATACTAAA	GCTTTGTATGCAACAAAGACTCTTCGAAAGAAGACGTTCTGCTCCGAAATCAGGTGGCT 1740 			GATATGAGCCTATTAATTAGAATGGCCATCTTTCCTGAAAATCTGGCACGATCTAC 1 	ATAGCAGAACITACCTGTGCAGTTGAAAGTGTTCATAAAATGGGTTTTATTCATAGAGA 1980 	ATTAAACCTGATAACATTTGATGACCGTGATGGCCATATTAAATTGACTGAC		CGGCAAGATAGCATGGATTTCAGTAACGAATGGGGAGATCCTTCCAATTGTCGGTGTGGG 2160 	GACAGACTGÁAGCCACTGGAGCGGAGAGCTGCTCGCCAGCACCAGCGATGTCTAGCCCAT 2220	TCTCTGGTTGGGACTCCCAATTATATGCACCTGAAGTGCTACTGCGAACAGGATATACA 2280	CAGCTGTGACTGGTGGAGTGTTGGTGTTATTCTTGTGAAATGTTGGTGGGACAACT 2340 	CCTTTCTTGGACAAACCCATTAGAAACACAAATGAAGGTTATCATCAGGAAACTTCT 2400 	CTACACATCCCTCCTCAAGCTAAGCTGAGTCCTGAAGCCTCTGACCTCATTATCAAACTG 2460 	TGTCGAGGACCAGAAGACCGCCTCGGCAAGAACGGTGCTGATGAGATAAAGGCTCATCCA 2520 	TTTTTTAAGACCATCGATTTCTCTAGTGATCTGAGACAGĆAGTCTGCTTCATACATCCCT 2580 	AAAATCACGCATCCAACAGATACATCCAATTTCGACCCTGTTGATCCTGATAAATTGTGG 2640 	AGCGATGGCAGCGAGGAAAATATCAGTGACACTCTGAGCGGATGGTATAAAAATGGG 2700 
ph 156		Qy 1681 Db 1681	Oy 1741 Db 1741	Qy 1801 Db 1801	Oy 1861 Db 1861	Qy 1921 Db 1921	Oy 1981 Db 1981	Oy 2041 Db 2041	Oy 2101 Db 2101	Oy 2161 Db 2161	Qy 2221 Db 2221	Oy 2281 Db 2281	Oy 2341 Db 2341	Qy 2401 Db 2401	Oy 2461 Db 2461	Oy 2521 Db 2521	Oy 2581 Db 2581	Oy 2641 Db 2641

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AACTAGGAGATCATTGTAAGAATTTGCAAGAGGCCTGAAGTGCAGGGGT 2940
                                                                                                                                                                                                                                                                                                                                                       PAGGITATGGGAAATTGTTTTAAAATGTTAATTTATTCCACCCTTTTAA 3060
                                                                                                                                                                                                                                                                                                                                                                                                          GAAAAAATTGTTATAAGGAAAGTAAATTATGAACTGAGTATTATAGTC 3120
                                                                                                                                                                                                                                                                                                                                                                                                                          SCACGCTTTCTATGAGTTCACCTTTCGGAGGTTTTTTGATGACAATGGC 2760
                                                                 TTATCCAAAGCCTATTGAGTATGAATACATTCATTCACAGGGCTCAGAA 2820
                                                                                                                                                                                                                                                                    IGAGAAAATTATGCAAATGTGACAGAGTTTGTGTGTGCTCTGTGTACAATA 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITAAAGTACITAAAAAGAGAAGCCIGGIAICIIIIGIAIAIAATAA 3180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ne; large tumour suppressor; fetal brain;
hreonine kinase; cell proliferation; antisense;
e; cancer; degenerative disorder; trauma;
y; therapy; antitumour; vulnerary; diagnostic;
transgenic animal; growth; senescence; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fing large tumour suppressor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1.2889
/*tag= a
/product= m-lats protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d; cDNA; 3213 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5WO-US04101.
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WPI; 1996-455275/45.

R P-PSDB; AAM05179.

XX

New isolated large tumour suppressor gene - used to develop prods.

PT for inhibiting cell proliferation or for enhancing proliferation

XX

XX

XX

XX

XX

This sequence encodes a mouse large tumour suppressor m-lats protein,

and has been isolated from a newborn mouse brain phage lambda-ZAP

CC CDNA library using a 2.2-kb DNA probe from the Drosophila lats gene

CC (AT42117). A homologous mouse sequence has also been isolated

CC (AT42117). A homologous mouse sequence has also been isolated

CC (AT42117). A homologous mouse sequence has also been isolated

CC (AT42117). A homologous mouse sequence has also been isolated

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CC (AT42117). A homologous mouse sequence has look been isolated

CC (AT42117). A homologous mouse sequence or inhibitors of caterial role throughout development. Activators or inhibitors of late fragment) may be used in therapy of cancer or other.

CC lates fragment by eused in therapy of cancer or other.

CC deficiency, etc., and fragments of the gene may be used as diagnostic probes. A lats-inhibitor sequence may be expressed in a transgenic probes. A lats-inhibitor sequence may be expressed in a transgenic senescence:

XX

Sequence 3213 BP; 946 A; 762 C; 697 G; 808 T; 0 other;
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241 CCACCACCTCCGAGAGGCCAGACCCCACCTCCCCGAGGCACCACTCCCCCTCCCCCTCA 300 61 CAGAGACACGGCCCATCTCTAGGAGAAATGTGGTTTATCGTTCTGAAAGCCCCAACTCA 120 121 CAGGCGGATGTAGGAAGACCTCTGTCTGGATCCGGCATTGCAGCATTTGCTCAAGCTCAC 180 CCAAGCAATGGACAGAGAGTGAACCCCCCACCACCACCTCAAGTTAGGAGTGTTACTCCT 240 9 9 0; Gaps 1 GIGCAACATICAATIAACCGAAAACAAAGCIGGAAAGGIICIAAAAGAGTICTAAGIICCI 1 GTGCAACATTCAATTAACCGAAAACAAAGCTGGAAAGGTTCTAAAGAGTCTCTAGTTCT 99.9%; Score 3209.8; DB 17; Length 3213; 99.9%; Pred. No. 0; Live 0; Mismatches 2; Indels 0; 0 Best Local Similarity 99.9 Matches 3211; Conservative Query Match 181

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> ACTCGGCAGCCACCTCCATATCGTCTGACCCAGCTAATGGACAAAAGCCCTCTGCT 660 CAACCCATCATCATGCAGAGTACTAGCAAATTTAACTTTACACCAGGGCGACCTGGAGTT 540 480 541 CAGAATGGTGGTGGTCAGTCTGATTTTATCGTGCACCAAAATGTCCCCACTGGTTCTGTG 600 301 TGGGAACCAAGCTCTCAGACAAAGCGCTACTCTGGGAACATGGAGTACGTAATCTCCCGA ATCTCCCCTGTTCCACCTGGGGGGTGGCAGGGGGTACCCTCCACCACCTCTTACCACT TCTCCCATGAATCCCCCTAGCCAGGCTCAGAGGGCCATTAGTTCTGTTCCAGTTGGTAGA 361 541 601 181 601 361 421 8 ò g g q ŏ g ò pp ð ò

oy du	661	ACCATCATTCGCC 
Qy Db	721	SATGGTGCCCAACAGGAACAGTCATAACATGGAGCTTTATAATATTAATGTCCCTGGA 78
Qy	781	DAAACAGCCTGGCCCCAGTCGTCTCTGCTCCTGCGCAGTCAT 
Oy Dp	4 4	TGAAATTCCTACATGGCAACCTAACATACCAGTGAGGTCAAATTCTTTTAATAACCCA 90 
QY	901	76CC 16CC 16CC
OY Db	961	CTCCTATTCAACAGCCGTGAAAAGCATGCGCGTCCTGAAACCAGAGCTG 
Oy Db	1021	rcag IIII rcag
QY Db	1081	TGAA   [   ]   TGAA
Qy	1141	CCCA
Qy Db	1201	ACCC  - -  ACCC
O. O.	1261	GAAA 1111 GAAA
Oy Dp	1321	AGAG           AGAG
QY	1381	AGAG        AGAG
QY	1441	AATG
S oy	1501	GAAA
S oy	ת תו	STCTAACTATATTGGTCTTAAAAGGGCTAAAATGGACAAGTCTATGTTGTAAAGATA 
QY	9 9	PATTAGGAATAGGACGTTTGGTGAAGTCTGTCTAGCAAGAAAAGTCG 
δλ	1681	CETATGCAACAAAGACTCTTCGAAAGAAAGACGTTCTGCTCCGAAATCAGGTGGCT
QQ A	1681	GCTTTGTATGCAACAAGACTCTTCGAAAGAACGATCTCTGCTCCGAAATCAAGTCGCTCTTGTTGAAAGCGGAAAGCGGAATATCCTAGCAGAAGCCGACAATGAGTGGGTGG

qq		——————————————————————————————————————	Db 2821 CAACAGTCTGATGAAGATGATCAACACACAGGTCCGATGGAAACAACGGAGATCTAGTG 2880
م م	01 TACTACTCTTCCAGGACAAGGACAACTTGTACTTTGTGATGGACTACATTCCTGGGGGG	О П	OY 2881 TATGTTAATAACTAGGAGATCATTGTAAGAATTTGCAAGAGGCCTGAAGTGCAGGGGT 2940  DD 2881 TATGTTTAATAACTAGGAGATCATTGTAAGAATTTGCAAGAGCCTGAAGTGCAGGGGT 2940
3 · 6 · 5	861 GATATGATGACCTATTAATTAGAATGGCATCTTTCCTGAAAATCTGCAGAGAGTGCAGAGAGAG	ζΟ qα	QY 2941 TTTTGAAGTTTTGAGAAAATTATGCAAATGTGACAGAGTTTGTGTGCTCTGTGTACAATA 3000
	861 GATAFGATGAGCCTATTAATTAGAATGGGGGTTCTFTCCTGAAAATCTGGGAGGTTTTAC 921 ATAGCAGAACTTACCTGTGCAGTTGAAAGTGTTCATAAAAGGGTTTTATTCATAGAGAT. 111111111111111111111111111111111111	О. П	OY 3001 TITTATITCCTAAGTTATGGGAAATTGTTTTAAAATGTTAATTTATTCCACCCTTTTAA 3060   D 3001 TITTATTTCCTAAGTTATGGGAAATGTTTTAAAATGTTAATTATTTCCACCCTTTTAA 3060
0	1941 ATANCAGAACTTACCTGTGCAGTTGAAAGTGTTCATAAATGGGTTTTATTCATAGAGAT 1980  1981 ATTAAACCTGATAACATTTGATTGACGTGATGGCCATATTAAATTGACTGAC		OY 3061 TTCAGTAATTTAGAAAAATTGTTATAAGGAAAGTAAATTATGAACTGAGTATTATAGTC 3120 Db 3061 TTCAGTAATTTAGAAAAATTGTTATAAGGAAAGTAAATTATGAACTGAGTATTATAGTC 3120
QY		-	OY 3121 AATTCTTGGTACTTAAAGTACTTAAAAAGAGAAGCCTGGTATCTTTGTATATAATAA 3180  1111111111111111111111111111111111
Oy .	CGGCAAGATAGCATGGATTTCAGTAACGAATGGGGAGATCCTTCCAATTGTCGGTGGGG 		Oy 3181 ATAATTTTAAAATCCCAAAAAAAAAAAA 3213 
oy do	2161 GACAGACTGAAGCCACTGGAGGGGAGAGCTGCTGGCCAGCACCAGGGATGTCTAGCCCAT 2220	ш <b>а</b> , н,	RESULT 3 AAT42118 ID AAT42118 standard; CDNA; 3984 BP.
Oy Db	2221 TCTCTGGTTGGGACTCCCAATTATATTGCACCTGAAGTGCTACTGCGAACAGGATATACA 2280 2221 TCTCTGGTTGGGACTCCCAATTATATTGCACCTGAAGTGCTACTGCGAACAGGATATACA 2280	, a, x u ;	AA AC AAT42118; XX DT 31-JAN-1997 (first entry)
Oy Db	2281 CAGCTGTGTGACTGGTGGAGTGTTGTGTTGTTGTTGTGAAATGTTGGTGGGACAACCT 2340 2281 CAGCTGTGTGACTGGTGGAGTGTTGGTGTTGTTGTGAAATGTTGGTGGGACAACCT 2340		H-lats gene encoding large tumour suppressor. Human; h-lats gene; large tumour suppressor; fetal bi
Sp G	2341 CCTTTCTTGGCACAAACCCCATTAGAAACACAAATGAAGGTTATCATCTGGCAAACTTCT 2400 11111111111111111111111111111111111	<b>E. E. E. S.</b>	protein-serine/threonine-Kinase, dominant-negative, cancer; degene growth deficiency; therapy, antit transgenic plant; transgenic anim
Oy Dp	2401 CTACACATCCTCCTCAAGCTAAGCTGAGTCCTGAAGCCTCTGACCTCATTATCAAACTG 2460 1	NOKE.	Homo saplens.
Qy Dp	2461 TGTCGAGGCCAGAAGACCGCCTCGGCAAGAACGCTGCTGATGAGATAAAGGCTCATCCA 2520 2461 TGTCGAGGACCAGAAGACGCCTCGGCAAGAACGGTGCTGATGAGATAAAGGCTCATCCA 2520	1	•
Qy	2521 TTTTTTAAGACCATCGATTTCTCTAGTGATCTGAGACAGCAGTCTGCTTGATACATCCCT 2580 2521 TTTTTTAAGACCATCGATTTCTCTAGTGATCTGAGACAGCAGTCTGCTTCATACATCCCT 2580		WO9630402-A1. 03-OCT-1996.
δλ Dp	2581 AAAATCACGCATCCAACAGATACATCCCACCCTGTTGATCCTGATAAATTGTGG 2640 		26-MAR-1996; 27-MAR-1995;
oy Op	2641       AGCGATGGCAGCGAGGAGAAATATCAGTGACACTCTGAGCGGATGGTATAAAAATGGG       2700         2641       AGCGATGGCAGGAGGAGGAAATATCAGTGACACTCTGAGCGGATGGTATAAAAATGGG       2700		Tao W
Qy Dp	2701 AAGCACCCCGAGCACGCTTTCTATGAGTTCACCTTTCGGAGGTTTTTTGATGACAATGGC 2760		WPI; 1996-455275/45. P-PSDB; AAW05178. New isolated large tumour suppress
Oy Dp	2761 TACCCATATAATTATCCAAAGCCTATTGAGTATGAATACATTCATT		for inhibiting cell proliferation or for Claim 6; Page 118-123; 215pp; English.
δŏ.			CC This sequence encodes a human large tumour suppressor h-lats protein, CC and has been isolated from a fetal human brain phage lambda-gt10. CC cDNA library using a 2.1-kb DNA probe from the mouse m-lats gene

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AAAGTACTTAAAAAGAGAGGCCTGGTATCTTTTGTATATAATAA 3180
                                                                                                                                                                                                                                                                                                                                               AGATGATCAACACACACAGCTCCGATGGAAACAACCGAGATCTAGTG 2880
                                                                                                                                                                                                                                                     AAAAATTGTTATAAGGAAAGTAAATTATGAACTGAGTATTATAGTC 3120
                                                                                                         SAAAATTATGCAAATGTGACAGAGTTTGTGTGTGCTCTGTGTACAATA 3000
                                                                                                                                                                               STIATGGGAAATIGTTTTAAAATGTTAATTTTATTCCACCCTTTTAA 3060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumour suppressor gene - used to develop prods. Proliferation or for enhancing proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        large tumour suppressor; fetal brain;
sonine-kinas; cell proliferation; antisense;
cancer; degenerative disorder; trauma;
therapy; antitumour; vulnerary; diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ransgenic animal; growth; senescence; ds.
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(AAT42119). The full-length cDNA is present in plasmid pBS(KS)-h-lats. The gene encodes a putative protein serine/threonine-kinase, and inhibits cell proliferation and plays a crucial role throughout development. Activators or inhibitors of lats function (e.g. an antisense oligonuclectide or dominant-negative lats fragment) may be used in therapy of cancer or other proliferative disorders, degenerative disorders, trauma, growth deficiency, etc., and fragments of the gene may be used as diagnostic probes. A
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                                                                                                               lats-inhibitor sequence may be expressed in a transgenic plant farm animal to confer increased growth and inhibit senescence.
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Use of lats proteins, complexes of lats and cdc2 for treating cancer that is refractory to treatment by standard chemotherapy and radiation therapy, and disorders associated with aberrant levels of cdc2 activity
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GCTCTGTGTACAATATTTTATTTTCCTAAATTATGGGAAATCCTTTTAAAATGTTAATTT
                               ATTCCACCTTTTAATTCAGTAATTTAGAAAAAATTGTTATAAGGAAAGTAAATTATGAA
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                                                                                                                                                                                          Human Lats (large tumour suppressor) DNA
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/product= "Lats protein"
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Stewart RA;
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                                                                                                                               DNA;
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P-PSDB; AAY70390.
                                                                                                                              AAZ51505 standard;
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Turenchalk GS,
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18-AUG-1998;
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The present sequence is a DNA encoding human Lats (large tumour suppressor) protein which is a cell overproliferation inhibitor and angative regulator of cell cycle-dependent kinase dcd2/cyclin A. The present sequence is useful for treating cancer that is refractory to standard chemotherapy or radiation therapy such as hyperplasia, metaplasia, or dysplasia, and disorders associated with aberrant levels of cdc2 activity. Conditions treated by promoting cdc2 function include degenerative disorders, growth deficiencies, hypoproliferative disorders, physical trauma, lesions, and wounds. An animal model preferably a mouse, in which a lats gene has been disrupted by homologous recombination, e.g. a lats knock-out mouse, is used for screening compounds that can be used to treat or prevent cancer, particularly skin cancer, soft tissue sarcomas and ovarian tumours, and disorders

Claim 44; Fig 12; 134pp; English.

22238

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therapy 1631 1571 1451 1511 1211 897 957 CCACCACCACCACCAGAGGCCAGAGACTCCCCCTCCAAGAGGTACAACTCCACCTCCCCCTTCA 1031 420 480 540 657 717 777 597 240 360 791 CAGAGACACGCCCCATCTCTAGGAGAAAATGTGGTTTATCGTTCTGAAAGCCCCCAACTCA 120 851 180 911 971 9 Gaps GCTTTACAÁACAGGGGCTTCTGCTGCTCCACCATCGCCAATGGAAACGTTCCTCAG GGGCATGAAATTCCTACATGGCAACCTAACATACCAGTGAGGTCAAATTCTTTTAATAAC CAACCCATCATGCAGAGTACTAGCAAATTTAACTTTACACCAGGGGGACCTGGAGTT TCGATGATGGTGCCCAACAGGAACAGTCATÁACATGGAGCTTTATAATATTAATGTCCCT CAGAATGGTGGTGGTCAGTCTGATTTTATCGTGCACCAAAA.--TGTCCCCACTGGTTCT GTGACTCGGCAGCCACCACCTCCATATCCTCTGACCCCAGCTAATGGACAAAGCCCCTCT GGACTGCAAACAGCCTGGCCCCAGTCGTCTTCTGCTCCTGCGCAGTCATCCCCAAGCGGT GTGCAACATTCAATTAACCGAAAACAAAGCTGGAAAGGTTCTAAAGAGTCTCTAGTTCCT CAGGCGGATGTAGGAAGACCTCTGTCTGGATCCGGCATTGCAGCATTTGCTCAAGCTCAC CCACCACCICCGAGAGGCCAGACCCCACCTCCCCGAGGCACCACTCCCCCTCCCCTCA TGGGAACCAAGCTCTCAGACAAAGCGCTACTCTGGGAACATGGAGTACGTAATCTCCCGA ATCTCCCCTGTTCCACCTGGGGCGTGGCAGGGGGTACCCTCCACCACCTCTTACCACT TCTCCCATGAATCCCCCTAGCCAGGCTCAGAGGGCCATTAGTTCTGTTCCAGTTGGTAGA 732 GIGCAGCAATCAGTTAACCGCAAACAGAGCIGGAAAGGTTCTAAAGAATCCTTAGTTCCT CCAAGCAATGGACAGAGAGTGAACCCCCCACCACCACCTCAAGTTAGGAGTTACTCCT gene 15; Length associated with pituitary dysfunction e.g. luteinizing ho hypogonadotropic hypogonadism. The lats DNA is also used Indels 0 other; Mismatches 385; Sequence 3984 BP; 1280 A; 847 C; 798 G; 1059 T; DB 2483; No. 0; Score . ő 77.3%; nilarity 87.4%; Conservative C Best Local Similarity Matches 2769; Conserv Query Match 1272 1512 1632 1212 1452 838 868 598 658 1392 718 778 1032 1092 1152 1332 912 241 972 421 481 541 792 852 181 301 361 61 121 g qq g ò d ò g ò ga ò ò g ò В g g g ð g ò õ ò ò ò d g

1917 1977 2711 2037 2771 2411 1737 2471 1797 2531 1857 2591 2651 GGCTTGTGCACTGGCTTCAGATGGACACATGACTCCAAGTACTACCAGAGTGGGGATCAC 2097 1677 1557 2291 2351 2171 1077 GGGGATATGATGAGCCTATTAATTAGAATGGGCATCTTTCCTGAAAATCTGGCACGATTC TACATAGCAGAACTTACCTGTGCAGTTGAAAGTGTTCATAAAATGGGTTTTATTCATAGA 2232 ATGATGCGGGTTGGATTATCTCAAGATGCCCAGGATCAAATGAGAAAGATGCTTTGCCAA AAAGCTTTGTATGCAACAAAGACTCTTCGAAAGAAAGAAGGCGTTCTGCTCCGAAATCAGGTG CTGTACTACTTTTCCAGGACAAGGACAACTTGTACTTTGTGATGGACTACATTCCTGGG AAACAGATTACAACTTCACCTÄTCACTGTTCGGAAAAAACAAGAAAGATGAAGAACGAAGA GAGICICGGATICAGAGITACICCCCACAGGCCTITAAGITCTICAIGGAGCAGCACGIA 1498, ATGATGCGGGTTGGATTATCTCAAGATGCCCAGGATCAAATGAGAAAGATGCTTTGCCAG GCAATTACACCAGCTCCTATTCAACAGCCTGTGAAAAGTATGCGTGTATTAAAAACCAGAG GAAGCTCCAAGCTATCAAGGTCCACCACCGCCTTATCCAAAACATCTGCTACACCAAAAC GAAGCTCCAAACTATCAAGGACCACCACCACCTACCCAAAACATCTGCTGCACCAAAAC GAGAACGICCIGAAGICTCATCAGCAGCGICTGCATCGGAAGAAGAAGCAGCIAGAAAAIGAA GCCATCACACCGCTCCTATTCAACAGCCCGTGAAAAGCATGCGCGCTCCTGAAACCAGAG CCATCTGTCCCTCCATATGAGTCAGTAAGTAAGCCCTGCAAAGATGAACAGCCTAGCTTA CCCAAGGAAGATGATAGTGAGAAGAGTGCGGACAGTGGTGACTCTGGGGATAAAGAAAAG CAGCCTACCCCTTTTTCTGAGGGTACAGCTTCAAGTGTGCCTGTCATCCCACCTGTTGCT CIGCAGACIGCITIAGCCCCAACCCAICCITCIIGGAIGCCACAGCCAGITCAGACIGII 2352 2412 2592 1918 1978 2038 1558 2292 1618 1678 1738 2472 1798 2532 1858 2652 2172 1992 1318 1378 2112 1438. 1932 1258 2052 1692 1018 1752. 1078 1812 1138 1872 1198 928 d qq qq δ q ò g Q g ζ pp qq g ò q ò ŏ a δy δ q qqοy g δλ qq à q Qγ Op ŏ Вþ δ δ ŏ

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"contains 10 copies of GGC repeat, similar to repeats that undergo expansion in human diseases associated with neuronal phenotypes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the nucleotide sequence of a cDNA clone coding for a human orthologue, i.e. hWART1 (see AAY06526), of Drosophila non-receptor serine/threonine kinase WART. hWART1 cDNA was isolated from a human bone marrow cDNA library using PCR fragments of hWART1 as probes. 3 Polymorphisms were identified in the hWART1 gene: (1) at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding human orthologs of Drosophila WART proteins, used to identify specific modulators for treating cancer or for diagnosis
   CTGAATATTATAGTCAGTTCTTGGTACTTAAAGTACTTAAAATAAGTAG 3900
                                                                                                                                                                                                 hWART1; WART orthologue; human; signal transduction;
                                                                                                                                                                                                               protein kinase; cancer; tumour; diagnosis; therapy; ss.
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/note="Alu-J subfamily repeat motif"
7339.7344
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/note= "results in Ala/Gly change"
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/note= "silent polymorphism"
replace(3252.3253)
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6058..6
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                                                                                                                                                                   Human WART1 cDNA.
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                                                                         2832 CCACGGCAAGATAGCATGGATTTCAGTAATGAATGGGGGGATCCCTCAAGCTGTCGATGT
                                                                                                      CATTCTCTGGTTGGGACTCCCAATTATATTGCACCTGAAGTGCTACTGCGAACAGGATAT
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nucleotide 978, resulting in an Ala/Gly change; (2) at nucleotide 1840, silent; and (3) at nucleotides 3252-3253, comprising a deletion of 2 adenosines, resulting in a c-terminal truncation of mutation was observed in 2 independent clones from human bone marrow cDNA. Truncation of hWART1 could play a role in disease progression. hWART1 shows strong expression in cell lines from non-small cell lung cancer, ovarian tumours, central nervous system tumors, renal tumours and breast tumours, and may provide a target for oncology drug development. Nucleic caids encoding full-length hWART1 and hWART1 polypeptides lacking one or more of amino acid segments 12.45, 55-151, 336-377, 404-520, 555-559, 601-702, 691-998 and 1011-1066, or lacking one or more of the N-terminal domain, catalytic domain, or C-terminal domain are claimed, as well as MARRY Sequences (AAX87397), NAMRIT and NAMRIZ DOTYPEPTIGES, antibodies, a method for identifying modulators of NAMRT function, and use of such modulator compounds to treat an abnormal condition involving hWART signal transduction, especially cancer. detection of hWART nucleic acids are also claimed. 

Sequence 7382 BP; 2291 A; 1458 C; 1417 G; 2216 T; 0 other;

1015 1135 1195 1315 1495 360 480 240 300 420 597 180 CAGAGACACGCCCCATCTCTAGGAGAAATGTGGTTTATCGTTCTGAAAGCCCCCAACTCA 120 9 AFCTCTCCCACCTGGGGCATGGCAAGAGGGCTATCCTCCACCACCTCTCAACACT GCTTTACAAACAGGGGCTTCTGCTGCTCCACCATCGTTCGCCAATGGAAACGTTCCTCAG CAACCCATCATCATGCAGAGTACTAGCAAATTTAACTTTACACCAGGGCGACCTGGAGTT CAGAATGGTGGTCGTCTGATTTTTATCGTGCACCAAAA---TGTCCCCACTGGTTCT GTGCAACATTCAATTAACCGAAAACAAAGCTGGAAAGGTTCTAAAGAGTCTCTAGTTCCT CAGGCGGATGTAGGAAGACCTCTGTCTGGATCCGGCATTGCAGCATTTGCTCAAGCTCAC CCAAGCAATGGACAGAGAGTGAACCCCCCACCACCACCTCAAGTTAGGAGTGTTACTCCT TGGGAACCAAGCTCTCAGACAAAGCGCTACTCTGGGAACATGGAGTACGTAATCTCCCGA ATCTCCCCTGTTCCACCTGGGGCGTGGCAGGAGGGGTACCCTCCACCACCTCTTACCACT TCTCCCATGAATCCCCCTAGCCAGGCTCAGAGGGCCCATTAGTTCTGTTCCAGTTGGTAGA GTGACTCGGCAGCCACCTCCATATCCTCTGACCCCAGCTAATGGACAAAGCCCCTCT 77.2%; Score 2481.4; DB 20; Length 7382; 87.3%; Pred. No. 0; Pred. No. 0; . 0; 0; Mismatches 386; Best Local Similarity 87.3 Matches 2768; Conservative Query Match 1016 1076 1256 1316 61 926 1136 1196 541 1436 1496 241 301 361 421 481 598 658 121 181 g g g q g ò qq ò ò ò ò ò ð 음 ö q ò a ò 8 ò g ð

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The invention relates to a human warts protein, homologous to Drosophila warts gene expression product. The warts expression product is a protein kinase involved in the regulation of proliferation and differentiation of epithelial calls and suppression of tumour formation. The gene, its expression product and antibodies are useful in the study of the mechanisms of tumour development. The present sequence represents a DNA
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                                      AGTGACACTCT-GAGCGGATGGTATAAAAATGGGAAGCACCCCGAGCACGCTTTCTATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1126.8; DB 20; Length 1374;
Pred. No. 8.5e-271;
0; Mismatches 147; Indels 1; 0
                                                                                                                                                                                                          gene fragment encoding a partial peptide fragment.
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                                                                                                                                                                                                                                                                                                                                                                              Saya
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                                                                           Gene of vertebrates homologous to a Drosophila gene
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                                                                                                                                                                                                                                                                                                                                                                              Niwa
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Matches 1226; Conserv
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ABA08740 standard; cDNA; 1357

ABA08740;

(first entry) 11-JAN-2002 Human large tumour suppressor 1 homologue cDNA, SEQ ID NO:516.

Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; proliferation; metastasis; cancer; tumour; haematopoietic disorder; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; cell culture; drug screening; infection; immune disorder; cell culture; drug screening; gene therapy; antinilammatory; antiathritic; antiathritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antillocer; ss. 

Homo sapiens

WO200157188-A2

09-AUG-2001

05-FEB-2001; 2001WO-US03800

03-FEB-2000; 2000US-0496914. 27-APR-2000; 2000US-0560875.

(HYSE-) HYSEQ INC

Tang YT, Liu C, Drmanac RT;

WPI; 2001-457740/49.

P-PSDB; ABB11496.

Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer

Claim 1; Page 554-555; 1963pp; English.

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA0825-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides.

To polypeptides in a sample, and methods of identifying compounds which the notypeptides of the invention. Although novel, many of the nucleotides polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence giving an insight into their probable biological activities, and hence giving an insight applications. The polypeptides of the invention may have various activities; stem cell growth factor activity; have various activities; stem cell growth factor activity; immunomodulatory activity; tissue growth activity; immunomodulatory activity; tissue growth activity; immunomodulatory activity; activin or inhibin related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombotytic activities; or may be

2202 CCAGCGAIGTCTAGCCCAITCTCTGGITGGGACTCCCAATIATATATGCACCTGAAGTGCT 2261

2082 CCAGAGTGGGGATCACCCACGGCAAGATAGCATGGATTTCAGTAACGAATGGGGAGATCC 2141

2142 TTCCAATTGTCGGTGTGGGGACAGACTGAAGCCACTGGAGCGGAGGGTGCTGCTGCCAGCA 2201

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involved in oncogenesis, cancer cell proliferation or metastasis.

Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, heamatopoletic discorders (e.g., myelolid or lymphoid cell cancers, heamatopoletic discorders (e.g., myelolid or lymphoid cell cancers, heamatopoletic discorders (e.g., myelolid or lymphoid cell proliferative retinopathy, atherosclerosis, coronary heart disease, proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischemina, bone disorders (e.g., osteoporosis), and abnormal vacular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound health in functions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders.

Colypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuropithalial cells may be used in cell growth.
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                                                                                                                                                                                                                                                                                                                               that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides and may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.
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Pred. No. 3.8e-242;
0; Mismatches 180;
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Best Local Similarity 85.7%;
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                         ACTGCGAACAGGATATACACAGCTGTGTGACTGGTGGTGTTGTTATTCTTTGTGA
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                                                                                                                                                                                                                                                                                     gene - used to develop prods for enhancing proliferation
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                                                                                                                                                                                                                                                                                                                                                                                                                    sequence encodes a mouse large tumour suppressor m-lats2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         o. A lats-inhibitor sequence may be expressed in a tra
or farm animal to confer increased growth and inhibit
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Mismatches 644;
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                                                                                                                                                                                                                                                                                                                                                           Claim 8; Page 133-137; 215pp; English.
                                                                                                                                                      Zhang
                                                                                                                                                                                                                                                                                  New isolated large tumour suppressor
for inhibiting cell proliferation or
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Matches 1237; Conserv
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26-MAR-1996;
                                                   27-MAR-1995;
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                                                             1504 CGGGTTGGATTATCTCAAGATGCCCAGGATCAAATGAGAAAGATGCTTTGCCAGAAAGAG
                                                                          1585 AAAGÇIGGGCICTGTGAGGCCGAGCAGAGCAGATGAGGAAGATCCTCTACCAGAAGGA.
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CACCCCGAGCACGCTTTCTATGAGTTCACCTTTCGGAGGTTTTTTGATGACAATGGCTAC 2763
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/note= "This region is erroneously repeated in the
mouse Lats2 DNA sequence shown in figure 14"
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/note= "This region is missing in the mouse Lats2
DNA sequence shown in figure 14"
                    ATCACGCATCCAACAGATACATCCAATTTCGACCCTGTTGATCCTGATAAATTGTGGAGC
                                                                                       GATGGCAGCGAGGAGGAAAATATCAGTGACACTCTGAGCGGATGGTATAAAAATGCGAAG
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treating cancer

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Use of lats proteins, complexes

actory to treatment by standard chemotherapy and radiation disorders associated with aberrant levels of cdc2 activity refractory and

Pages 112-117; 134pp; English 44: Claim

The present sequence is a DNA encoding mouse Lats2 (large tumour suppressor) protein which is a cell overproliferation inhibitor and a negative regulator of cell cycle-dependent kinase cdc2/cyclin A.

The present sequence is useful for treating cancer that is refractory to standard chemotherapy or radiation therapy such as hyperplasia, or dysplasia, and disorders associated with aberrant levels of cdc2 activity. Conditions treated by promoting cdc2 function include degenerative disorders, growth deficiencies, hypoproliferative disorders, physical trauma, lesions, and wounds. An animal model preferably a mouse, in which a lats gene has been disrupted by homologous recombination, e.g. a lats knock-out mouse, is used for screening compounds that can be used to treat or prevent cancer, particularly skin cancer, soft tissue sarcomas and ovarian tumours, and disorders associated with pituitary dysfunction e.g. luterhizing hormone (LH) hypogonadotropic hypogonadism. The lats DNA is also used in gene therapy.

Sequence 3155 BP; 751 A; 924 C; 894 G; 586 T; 0 other;

Length 3155; Indels DB 21; Score 812.6; DB 21; Pred. No. 3.3e-192; 0; Mismatches 644; 25.3%; 65.1%; Similarity

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1158 CAACCTGAGCCTCACTGCCCGCCCCAACACGTCACCGCCGTGACGCCGCACACTTC 1044 CAACAGCCCGTGAAAAGCATGCGCGTCCTGAAACCAGAGCTGCAGACTGCTTTAGCCCCCA 1038 CCACCACCACCTTATCCAAAACATCTGCTACAACAAACCCATCTGTCCCTCCATATGAG 1218 ACCCATCCTTCTTGGATGCCACAGCCAGTTCAGACTGTTCAGCCTACCCCTTTTTCTGAG 1098 GAGGGCAGCCCACACCCCCTGGATGTGGACTATGGCGGCTCCGAGCGCAGTGC 1224 CACTCTGCTAATTCTCAGCCTTCTGCCACTACAGTCACTGCCATCACACCCGCTCCTATT 978 1105 TCGCACCCCGCCTGGGTGGCTGGCTGGCCCACAGCCTGCACTGGAGAGGAGGAAG GGTACAGCTTCAAGTGTGCCTGTCATCCCACCTGTTGCTGAAGCTCCAAGGT Matches 1237; Conservative 1045 1039 1165 985 979 1099 919 g g g ò ò ò ٠Ş g ò

1323 1383 TCAGTAAGTAAGCCCTGCAAAGATGAACAGCCTAGCTTACCCAAGGAAGATGATAGTGAG 1278 GACCTGGACAGCCTGTGCACCAGTGTGCAGCAGAGGCGCACTGGATCTAGAC 1344 GGGAGTGACAAGAGCCACAAAGGTGCGAAGGGAGACAAAGCTGGCAGAGAAAAAAGCAG 1404 ATTACAACTTCACCTATCACTGTTCGGAAAAACAAGAAGATGAAGAACGAAGAGTCT AAGAGTGCGGACAGT 1219 1345 1285 1279 1324 ö g δ q ò

CCACCGCCTCCGTATCCAAAGCACTTGCTGCTGCCCAGTAAGTCTGAGCAGTACAGCGTG :1284

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CGGATTCAGAGTTACTCCCCACAGGCCTTTAAGTTCTTCATGGAGCAGCACGTAGAGAAC 1405 1384

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GTCCTGAAGTCTCATCAGCAGCGTCTGCATCGGAAGAAGCAGCTAGAAAATGAAATGATG CGGGTTGGATTATCTCAAGATGCCCAGGATCAAATGAGAAAGATGCTTTGCCAGAAAGAG 1444 1525 1504

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ATCACGCATCCAACAGATACATCCAATTTCGACCCTGTTGATCCTGATAAATTGTGGAGC

GATGGCAGCGAGGAAAATATCAGTGACACTCTGAGCGGATGGTATAAAAATGGGAAG

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TCTAACTATATTCGTCTTAAAAGGGCTAAAATGGACAAGTCTATGTTTGTAAAGGATAAAG 1623

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1803 1863 2043 2103 2283 2343 2403 2463 2583 1824 ATGATGAGCCTATTAATTAGAATGGGCATCTTTCCTGAAAATCTGGCACGATTCTACATA 1923 2004 GCAGAACTTACCTGTGCAGTTGAAAGTGTTCATAAAATGGGTTTTATTCATAGAGATATT 1983 2064 2124 2163 2244 2223 2304 2364 2424 2484 2544 2523 CTGGTTGGGACTCCCAATTATATTGCACCTGAAGTGCTACTGCGAACAGGATATACACAG CTTGTCGGGACACCAAATTACATCGCTCCGGAGGTGCTTCTCCGCAAGGGTACACGCAG TTCTTGGCACAAACCCCATTAGAAACACAAATGAAGGTTATCATCTGGCAAACTTCTCTA TICTTGGCCCCCACCCCACAGAGACGCAGCTGAAGGTGATCAACTGGGAGAGAGCACGCTG TTGTATGCAACAAAGACTCTTCGAAAGAAAGACGTTCTGCTCCGAAATCAGGTGGCTCAT TACTCTTTCCAGGACAAGGACAACTTGTAATTGTGATGGACTACATTCCTGGGGGGGAT AAACCTGATAACATTTTGATTGACCGTGATGGCCATATTAAATTGACTTTGGCTTG AGACTGAAGCCACTGGAGCGGAGGTGCTCGCCAGCACCAGCGATGTCTAGCCCATTCT CTGTGTGTGACTGGTGTTGGTGTTATTCTTTGTGAAATGTTGGTGGGACAACCTCCT CACATCCCTCCTCAAGCTAAGCTGAGTCCTGAAGCCTCTGACCTCATTATCAAACTGTGT TGCGCGGCTGACTGCCGCCTGGGCAGGGATGGGGCAGATGACCTCAAGGCACACCCGTTC TITAAGACCATCGATTTCTCTAGTGATCTGAGACAGCAGTCTGCTTCATACATCCCTAAA ACATTAGGAATAGGAGCGTTTGGTGAAGTCTGTCTAGCAAGAAAAGTCGATACTAAAAGCT ACTCTAGGCATCGGTGCCTTTGGGGAAGTGTGCCTCGCTTGTAAGCTGGACACTCACGCT TGCACTGGCTTCAGATGGACACATGACTCCAAGTACTACCAGAGTGGGGATCACCCACGG CAAGATAGCATGGATTTCAGTAACGAATGGGGAGATCCTTCCAATTGTCGGTGTGGGGAAC CGAGGACCAGAAGACCGCCTCGGCAAGAACGGTGCTGATGAGATAAAGGCTCATCCATTT 1645 1705 2125 2344 1624 1744 1804 1864 1924 2002 2065 2044 2185 2164 2245 2224 2305 2284 2365 2425 2485 1684 1984 2104 2404 2464 g Q g ò Dp δ g δ ద ò qq δ g ò g ò g δy g δ g δ g ŏ g δ g Ö .g ò Db å )

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Sequence 5276 BP; 1348 A; 1407 C; 1345 G; 1176 T; 0 other;
                                                                                Best Local Simi
Matches 1099;
                                                         Query Match
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                  2725 GAGGCCAGCGAGAG---AGCGCCAAGGCCTGGGACACGCTGGCCTCCCCCAGCAGCAAG 2781
                                                                                         New nucleic acid encoding human orthologs of Drosophila WART proteins, used to identify specific modulators for treating cancer or for diagnosis
                                                             CACCCCGAGCACGCTTTCTATGAGTTCACCTTTCGGAGGTTTTTTGATGACAATGGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WART2; hWART2; WART orthologue; human; signal transduction; protein kinase; cancer; tumour; diagnosis; therapy; ss.
                                                                                                                                                    2764 CCATATAATTATCCAAAGCCTATTGAGTATGAATACATT 2802.
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                                                                                                                                                                                                                                                                                                             AAX87397 standard; cDNA; 5276 BP
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P-PSDB; AAY06527.
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                                                                                                                                                                                                                                                                                                                                                              2227 AGCAGAAGGITAACCGGAGGCTGCAGCTGGAGCAAGAAATGGCCAAAGCTGGACTCTGTG 2286
                                                                                                                                 1220 CAGTAAGTAAGCCCTGCAAAGATGAACAGCCTAGCTTACCCAAGGAAGATGATAGTGAGA[1279
                                                                                     1987 CAGGCATGGAGGCCTCCGTGCGGGCCCCAACGAGGCCGGAGGGCGGCGACAAGAGCC 2046
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                                                                                                                                                                                                 TCACTGTTCGGAAAAACAAGAAGATGAAGAACGAAGAGAGTCTCGGATTCAGAGTTACT
                                                                                                                                                                                                                                                                  CCCCACAGGCCTTTAAGTTCTTCATGGAGCAGCACGTAGAGAACGTCCTGAAGTCTCATC
                                                                                                                                                                                                                                                                                 Length 5276;
                                  Indels
 Score 787.2; DB 20;
Pred. No. 9.2e-186;
0; Mismatches 498;
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0
      24.5%;
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                        Similarity
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  ATTATATATGCACCTGAAGTGCTACTGCGAACAGGATATACACAGCTGTGTGACTGGTGGA
                               GTGTTGGTGTTATTCTTTGTGAAATGTTGGTGGGACAACCTCCTTTCTTGGCACAAACCC
                                                                                                                                                                                                                      CATTAGAAACACAAATGAAGGTTATCATCTGGCAAACTTCTCTACACATCCCTCCTCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; growth hormone inhibited tumour suppressor protein; he antineoplastic; dwarfism; dyapantism; acromegaly; anglopathy; diabetic nephropathy; cardiopathy; tumour; breast cancer; renal adenocarcinoma; colorectal cancer; leukaemia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "tumour suppressor protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding a tumour suppressor protein hGHITS1
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                                                                                    New human growth hormone inhibited tumour suppressor genes 1 and 2 diagnosis of dwarfism, gigantism, acromegaly, anglopathy, diabetic nephropathy or cardiopathy
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                                                                                                                                                                                        The present sequence encodes a human growth hormone inhibited tun suppressor (hGHITS) protein. The hGHITS proteins can be used in antineoplastic pharmaceutical preparation. Probes for the hGHITS
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Pred. No. 9.4e-186;
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68.7%;
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Matches 1099; Conservative
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                Kono K,
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Human, growth hormone inhibited tumour suppressor protein; hGHITS; antineoplastic; dwarfism; gigantism; acromegaly; angiopathy; diabetic nephropathy; cardiopathy; tumour; breast cancer; renal adenocarcinoma; colorectal cancer; leukaemia; ss.

encoding a tumour suppressor protein hGHITS2

"tumour suppressor protein"

/rtag= a /product= 387..3653 /\*tag= A

EP1022333-A1

26-JUL-2000

Location/Qualifiers

Homo sapiens

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              1940 CAGTTGAAAGTGTTCATAAAATGGGTTTTTATTCATAGAGATATTAAACCTGATAACATTT
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for

s 1 and 2 diabetic

owth hormone inhibited tumour suppressor genes dwarfism, gigantism, acromegaly, angiopathy, o

FN;

Zolotaryov

Kono K,

Koga J,

WPI; 2000-516013/47. P-PSDB; AAB07664.

(JCRP-) JCR PHARM CO LID

99EP-0119199 99JP-0016223

07-OCT-1999;

25-JAN-1999;

New human growth hormone inhibited tumour diagnosis of dwarfism, gigantism, acromega

Claim 1; Page 28-39; 59pp; English.

nephropathy or cardiopathy

1220 CAGTAAGTAAGCCCTGCAAAGATGAACAGCCTAGCTTACCCAAGGAAGATGATAGTGAGA 1279 1999 CAGGCATGGAGCAGAGCCTCCGTGCGGGCCCCAACGAGCCCGAGGGCGGCGACAAGAGCC 2058 The present sequence encodes a human growth hormone inhibited tumour suppressor (hGHITS) protein. The hGHITS proteins can be used in an antineoplastic pharmaceutical preparation. Probes for the hGHITS DNA sequences can be used in diagnostic pharmaceutical preparations. The diagnostic pharmaceutical preparations can be used for examining expression of hGHITS genes in dwarfism, gigantism, acromegaly, angiopathy, diabetic nephropathy or cardiopathy, or in malignant tumours including breast cancer, renal adenocarcinoma, colorectal cancer, and leukaemia. Antibodies against the proteins can be used in diagnostic pharmaceutical preparation for examining expression of 2059 GCAAAAGCGCCAAGGGGGACAAAGGCGGAAAGGATAAAAAGCAGATTCAGACCTCTCCCG AGCAGCGTCTGCATCGGAAGAAGCAGCTAGAAAATGAAATGAAATGCGGGTTGGATTATCTC 1340 TCACTGTTCGGAAAAAAAAAAAAAGATGAAGAACGAAAGAAGAGTCTCGGATTCAGAGTTACT CCCCACAGGCCTTTAAGTTCTTCATGGAGCAGCACGTAGAGAACGTCCTGAAGTCTCATC DB 21; Length 5486; Sequence 5486 BP; 1380 A; 1451 C; 1388 G; 1267 T; 0 other; Indels Score 787.2; DB 21; Pred. No. 9.4e-186; ); Mismatches 498; ;0 24.5%; a diagnostic pharmaccara tumour suppressor gene. Conservative Query Match Best Local Similarity Matches 1099; Conserv 1400 2179 1460 q ŏ g

2239 δy g ŏ ŏ

(first entry)

07-NOV-2000

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DNA;

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 AAGATGCCCAGGATCAAATGAGAAAGATGCTTTGCCAGAAAGAGTCTAAACTATATTCGTC 1579
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proteins having kinase activity. The kinase polypetides and fragmented polypeptides are used as molecular weight and isoelectric focusing markers, and as controls for peptide fragmentation. They also have a number of therapeutic uses as kinases play a central role in cellular signal transduction. The polypeptides could also be used to identify binding partner proteins. The polypeptides can also be used a reagent to identify any proteins that the polypeptide requiates, and proteins with which it might interact. The polypeptides may also be used for preparation of antibodies. The antibodies can be used in assays to detect the presence of the protein, and to purify the protein by immunoaffinity chromatography.
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                                                                                                                                                                    Kinase activity; molecular weight marker; isoelectric focusing marker; peptide fragmentation control; cellular signal transduction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes a partial polypeptide which has kinase activity. The kinase polynucleotides can be used to express the polypeptides, and as probes to identify nucleic acids encoding
                                                                                            3436 GTAGCACCAAGGCCTGGGACACACTCACCTCGCCCAATAACAAGCATCCTGAGCACTCGCCCGT
2600 ATACATCCAATTTCGACCCTGTTGATCCTGATAAATTGTGGAGCGATGGCAGCGAGGAGG
                                    3379 ACACCTCGAATTTCGACCCCGTAGATGAAGAAGCCCTTGGAACGATGCCAGC ---GAAG
                                                                                                                                                TCTATGAGTTCACCTTTCGGAGGTTTTTTGATGACAATGGCTACCCATATAATTATCCAA
                                                                         2660 AAAATATCAGTGACACTCTGAGCGGATGGTATAAAAATGGGAAGCACCCCGAGCACGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human kinase polypeptides and polynucleotides used as weight markers and as controls for peptide fragmentation
                                                                                                                                                                                                                        AGCCTATTGAGTATGAATACATTCATTCACAGGGCTCAGA 2819
                                                                                                                                                                                                                                                           3556 AGCCTTCAGGAGCAGAGCTTCACAGGCTGAGAGCTCAGA 3595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoding a partial protein kinase.
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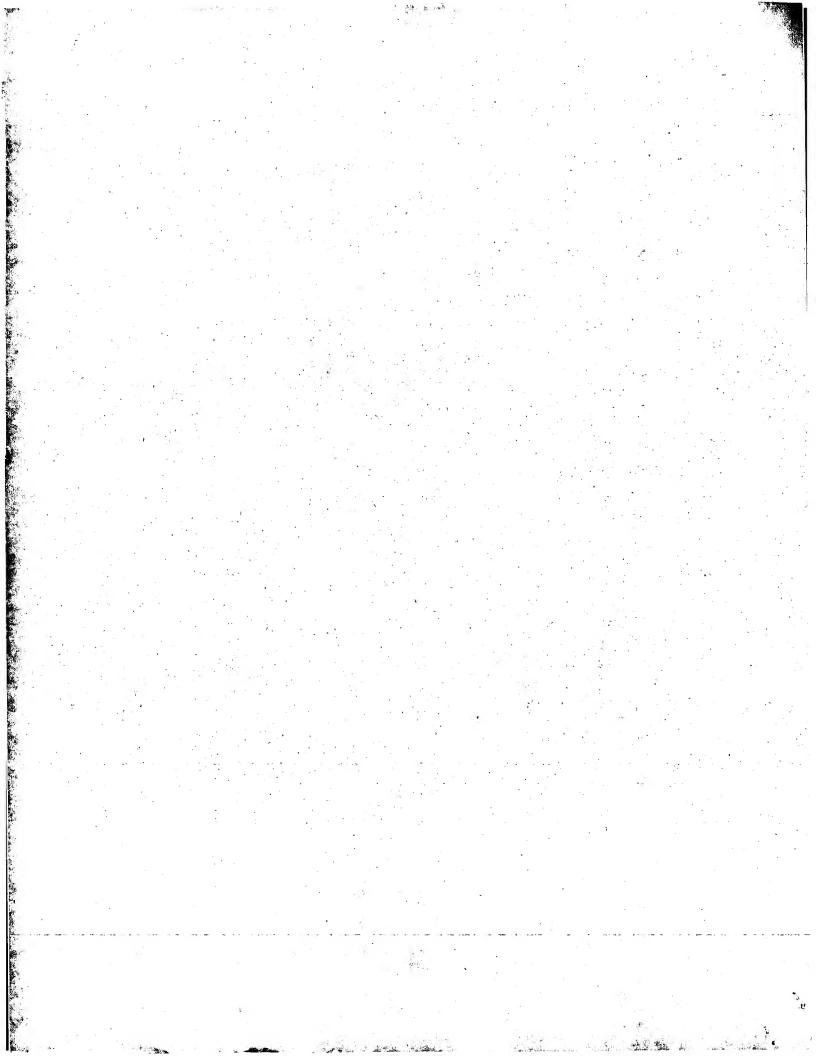
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T; 0 other;
                                          Score 785.6; DB 21;
Pred. No. 1.4e-185;
0; Mismatches 499;
  G; 368
  Sequence 1961 BP; 504 A; 550 C; 539
                                          24.5%;
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                                                                        Length 3533;
                                                                                             Indels
                                                  831 A; 1096 C; 1011 G; 595 T; 0 other;
                                                                     24.5%; Score 785.6; DB 22;
68.6%; Pred. No. 1.9e-185;
ive 0; Mismatches 499;
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                     Lats2 is
                                                                               Best Local Similarity
Matches 1098; Conserv
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Sequence 10, Patent No. 52 Sequence 1,

Sequence

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us-09-763-334-3.rni

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APPLICANT: Wang, Weiyi
APPLICANT: Zhang, Sheng
APPLICANT: Yu, Wan
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS
TITLE OF INVENTION: GENES AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/442,100
                                            US-08-422-706B-8
US-08-60-822A-61
US-09-005-069-61
US-09-171-156A-20
US-09-131-930-1
US-09-094-714A-48
US-09-025-749-24
US-09-429-322-3
US-09-430-564-1
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US-09-016-000-10
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US-09-212-771-1
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1: 1155 Avenue of the Americas
New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/09442100 Patent No. 6359193
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TELEFAX: (212) 869-9741/8864
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 652
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TELEPHONE: (212) 790-9090
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TYPE: nucleic acid
STRANDEDNESS: double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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APPLICANT: Xu, Tian
APPLICANT: Tao, Wufan
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CITY: Ne
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: / cgn2_6/ptodata/1/ina/6A_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: / cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*
                    GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                              441<sup>3</sup>62 segs, 153338381 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                     - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Gaps. 120 180 120 180 24.0 240 480 300 300 360 360 420 420 480 1020 09 09 540 540 600 900 099 720 1020 099 720 780 780 840 840 006 900 960 960 GTGCAACATTCAATTAACCGAAAACAAAGCTGGAAAGGTTCTAAAGAGTCTCTAGTTCCT GTGCAACATTCAATTAACCGAAAACAAAGCTGGAAAGGTTCTAAAAGAGTCTCTAGTTCCT CAGAGACACGGCCCATCTCTAGGAGAAAATGTGGITTAATGGTTTCTGAAAAGCCCCAACTCA CAGGCGGATGTAGGAAGACCTCTGTCTGGATCCGGCATTGCAGCATTTGCTCAAGCTCAC CCAAGCAATGGACAGAGAGTGAACCCCCACCACCACCTCAAGTTAGGAGTGTTACTCCT CCACCACCTCCGAGGCCAGACCCCACCTCCCCGAGGCACCACTCCCCCTCCACTCC TGGGAACCAAGCTCTCAGACAAAGCGCTACTCTGGGAACATGGAGTACGTAATCTCCCGA ATCTCCCCTGTTCCACCTGGGGCGTGGCAGGGGGGTACCCTCCACCACCTCTTACCACT TCTCCCATGAATCCCCCTAGCCAGGCTCAGAGGGCCATTAGTTCTGTTCCAGTTGGTAGA CAACCCATCATGCAGAGTACTAGCAAATTTAACTTTACACCAGGGCGACCTGGAGTT TTACAAACAGGGGCTTCTGCTGCTCCACCATCATTCGCCAATGGAAACGTTCCTCAGTCG ACTCGGCAGCCACCACCTCCATATCCTCTGACCCCAGCTAATGGACAAAGCCCCTCTGCT **ATGATGGTGCCCAACAGGAACAGTCATAACATGGAGCTTTATAATATTAATGTCCCTGGA** CTGCAAACAGCCTGGCCCCAGTCGTCTTCTGCTCCTGCGCAGTCATCCCCAAGCGGTGGG CATGAAATTCCTACATGGCAACCTAACATACCAGTGAGGTCAAATTCTTTAATAACCCA TTAGGAAGTAGAGCAAGTCACTCTGCTAATTCTCAGCCTTCTGCCACTACAGTCACTGCC **ATCACACCGGCTCCTATTCAACAGCCCGTGAAAAGCATGCGCGTCCTGAAACCAGAGCTG** Length 3213; ó Indels 4; . . DB Score 3213; Pred. No. 0; Mismatches ó 100.0%; 100.0%; Local Similarity 100. es 3213; Conservative Match Best Loca Matches -61 121 121 181 181 241 241 301 301 361 361 421 421 481 481 541 541 601 661 601 661 721 721 841 781 781 841 901 Query 901 196 961 ò a ŏ g ö a Op δ à g οy 8 QQ ô ò QQ ò a à a οy 임 à g ð g g à QQ à ò g ò

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GENES AND METHODS BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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Pred. No. 0;
     Pennie & Edmonds
1155 Avenue of the Americas
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                                                                                                  Sequence 3, Application US/09442100 Patent No. 6359193 GENERAL INFORMATION:
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(212) 869-9741/8864
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                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 65.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 77.3%;
Best Local Similarity 87.4%;
Matches 2769; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                     APPLICANT: Wang, Weiyi
APPLICANT: Zhang, Sheng.
APPLICANT: Yu, Wan
TITLE OF INVENTION: NUCLE
TITLE OF INVENTION: GENES
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DATA
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APPLICATION NUMBER:
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231..3623.
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APPLICANT: Tao, Wufan
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2101 CGCCAAGATAGCATGGATTTCAGTAACGAATGGGGAGATCCTTCCAATTGTCGGTGTGGG
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                                                                                                                                 TCTCTGGTTGGGACTCCCAATTATATTGCACCTGAAGTGCTACTGCGAACAGGATATACA
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-	11	241 CCACCACCTCC 	301 TGGGAACCAAG 	361 ATCTCCCCTGT             092 ATCTCCTGT	21	481 CAACCCATCAT	541 CAGAATGGTGG 	98	92	718 TCGATGATGT                452 TCTATGATGGT	778 GGACTGCAAACI 	838 GGGCATGAAAT 	32 8	9 2		e 0	8 2	an 01	58 CCCAAGGAAGAT
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1992 CCCAAGGAAGATGAGAGTGAAAAGAGTTATGAAAATGTTGATAGTGGGGATAAAGAAAG 2051 2111 1497 1557 1617 2351 1677 2411 1797 2531 2591 2651 1977 2711 2232 ATGATGCGGTTGGATTATCTCAAGATGCCCAGGATCAAATGAGAAAGATGCTTTGCCAA 2291 CTGTACTACTCTTTCCAGGACAAGGACAACTTGTACTTTGTGATGGACTACATTCCTGGG 1857 1858 GGGGATATGATGAGCCTATTAATTAGAATGGGCATCTTTCCTGAAAATCTGGCACGATTC 1917 2037 2217 3011 2771 2157 2891 2951 ACACAGCTGTGTGACTGGTGGTGTGTTATTCTTTGTGAAATGTTGGTGGGACAA 2337 AAACAGATTACAACTTCACCTATCACTGTTCGGAAAAACAAGAAGATGAAGAACGAAGA 1438 GAGAACGTCCTGAAGTCTCATCAGCAGCGTCTGCATCGGAAGAAGCAGCTAGAAAATGAA 1498 ATGATGCGGGTTGGATTATCTCAAGATGCCCAGGATCAAATGAGAAAGATGCTTTGCCAG 2532 CTATATTATTCATTCCAAGATAAGGACAAFTTATACTTTGTAATGGACTACATTCCTGGG 1918 TACATAGCAGAACTTACCTGTGCAGTTGAAAGTGTTCATAAAATGGGTTTTATTCATAGA 2652 TACATAGCAGAACTTACCTGTGCAGTTGAAAGTGTTCATAAAATGGGTTTTATTCATAGA 2098 CCACGGCAAGATAGCATGGATTTCAGTAACGAATGGGGAGATCCTTCCAATTGTCGGTGT 2158 GGGBACAGACTGAAGCCACTGGAGCGGAGAGCTGCTCGCCAGCACCAGCGATGTCTAGCC CATICICIGGITGGGACTCCCAATTATATTGCACCTGAAGTGCTACTGCGAACAGGATAT 1798 2172 1618 2352 1678 2412 2218 2278 염

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Patent No. 6359193
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Tao, Wufan
Wang, Weiyi
Zhang, Sheng
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TITLE OF INVENTION:
TITLE OF INVENTION:
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COUNTRY:

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1039 ACCCATCCTTCTTGGATGCCACAGCCAGTTCAGACTGTTCAGCCTACCCCTTTTTCTGAG 1098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAGTAAGTAAGCCCTGCAAAGATGAACAGCCTAGCTTACCCAAGGAAGATGATAGTGAG 1278
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Pred. No. 1.2e-211;
); Mismatches 644;
                             CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/no.
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;
                                                                                                                                                                                                                                                                                                               (212) 790-9090
(212) 869-9741/8864
               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                      NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 65,
TELECOMMUNICATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.3%;
                                                                                                                                                                                                                                                                                                                                                  TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 3155 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 1237; Conservative
                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
READABLE FORM:
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US-09-442-100-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                TELEFAX:
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		Oy 2584 A Db 2665 A	Oy. 2644 G			Oy 2764 C	RESULT 4 US-09-509-9	; Patent No ; GENERAL I ; APPLICAN ; APPLICAN	; APPLICAN ; APPLICAN ; TITLE OF ; FILE REF	CURRENT CURRENT NUMBER O SOFTWARE	; SEQ ID NO ; LENGTH: ; TYPE: D ; ORGANIS	Query Mat Best Loca	Matches 1 Oy 1220 C	1280	7	1		_ <del></del> 1	DB 415 A QY 1580 T	Db 475 T
· <del>-</del>			*						<ul><li>→ ±</li></ul>	(1)		8			*	. *		-		
	1444 GTCTGRAARGTGTGTATGAGGAGGTCTGCATGGAAGGAAGCTAAAAGGAAATGAATG	1504 CGGGTTGGATTAFCTCAAGATGCCCAGGATCAAATGAGAAAGATGCTTTGCCAGAAAGAG 1563 	TCTAACTATATTCGTCTTAAAAGGGCTAAAATGGACAAGTCTATGTTTGTAAAGATAAAG	TCTAACTACAACCGGCTGAAGAGGGCCAAGATGGACAGTCCATGTTTGTGAAATCAAG	1624 ACATTAGGAATAGGAGCGTTTGGTGAAGTCTGTCTAGCAAGAAAGTCGATACTAAAGCT 1683	1684 TTGTATGCAACAAAGACTCTTGGAAAGAAGACGTTCTGCTCCGAAATCAGGTGGCTCAT 1743 	GTGAAAGCGGAGAGGATATCCTAGCAGAAGCGGACATGAGTGGGTGG	1804 TACTCTFTCCAGGACAAGGACAACTTGTACTTTGTGATGGACTACATTCCTGGGGGGGG	1864 ATGATGAGCCTATTAATTAGAATGGGCATCTTTCCTGAAAATCTGGCACGATTCTACATA 1923 	1924 GCAGAACTTACCTGTGCAGTTGAAAGTGTTCATAAAATGGGTTTTATTCATAGAGATATT 1983   IIII   III   IIII   IIIII   IIII   IIII   IIII   IIII   IIII   IIII   IIII   IIII   IIIII   IIII   IIII   IIII   IIII   IIII   IIII   IIII   IIII   IIIII   IIII   IIII   IIII   IIII   IIII   IIII   IIII   IIII   IIIII   IIII   IIII	1984 AAACCTGATAACATTTTGATTGACCGTGATGGCCATATTAAATTGACTTTGGCTTG 2043 1	2044 IGCACTGGCTTCAGATGGACACATGACTCCAAGTACTACCAGAGTGGGGATCACCCAGG 2103 	2104 CAAGATAGCATGGATTTCAGTAACGAATGGGGAGATCCTTCCAATTGTCGGTGTGGGAC 2163 1	2164 AGACTGAAGCCACTGGAGCGGAGAGCTGCTCGCCAGCACCAGCGGATGTCTAGCCCATTCT 2233 11 1 11 1 1 1 1 1 1 1 1 1 1 1 1 1	2224 CIGGTIGGGACICCCAATTAȚATIGCACCIGAAGIGCIACTGCGAACAGGAIATACACAG 2283 	2284 CTGTGTGACTGGTGGTGTTGGTGTTATTCTTTGTGAAATGTTGGTGGACAACCTCCT 2343. 	2344 TICITGGCACAAACCCCATTAGAAACACAAATGAAGGTTATCATCTGGCAAACTTCTTA 2403	2404 CACATCCTCCTCAAGCTAAGCTGAGTCCTGAAGCTCTGACCTCATATCAAACTGTGT 2463 1	2464 CGAGGACCAGAGACGCCTCGGCAAGAACGGTGCTGATGAGATAAAGGCTCATCCATTT 2523	TTTAAGACCATCGATTTCTCTAGTGATCTGAGACAGCAGTCTGCTTCATACATCCTAAA
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NNT: Virca, Duke
NNT: Bird, Timochty A.
NNT: Marken, John S.
NNT: Marken, John S.
NNT: Marken, John S.
PERRENCE: 2877-US
APPLICATION HUMBER: US/09/509,902A
                                                                                                                                                                                            CACCCCGAGCACCACTTCTATGAGTTCACCTTTCGGAGGTTTTTGATGACAATGGCTAC 2763
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ATCACGCATCCAACAGATACATCCAATTTCGACCCTGTTGATCCTGATAAATTGTGGAGC 2643
                                                                       GAGGCCAGCGGAGAG---AGCGCCAAGGCCTGGGACACGCTGGCCTCCCCCAGCAGCAAG 2781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                      Score 785.6; DB 4;
Pred. No. 2.1e-204;
0; Mismatches 499;
                                                                                                                                                                                                                                                                   CCATATAATTATCCAAAGCCTATTGAGTATGAATACATT 2802
                                                                                                                                                                                                                                                                                                                                                                                       15, Application US/09509902A
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OF SEQ ID NOS: 16
:: Patentin Ver. 2.0
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68.6%;
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902A-15
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                                                                                                                                                                                                                                                                                                                                                                                                              o. 6387676
INFORMATION:
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                                                  CTCTTCGAAAGAAAGACGTTCTGCTCCGAAATCAGGTGGCTCATGTGAAAGCGGAGAGGG
                                                                  TCAGTAACGAATGGGGAGATCCTTCCAATTGTCGGTGTGGGGACAGACTGAAGCCACTGG
 CGTTTGGTGAAGTCTGTCTAGCAAGAAAAGTCGATACTAAAGCTTTGTATGCAACAAAGA
                AGGACAACTTGTACTTTGTGATGGACTACATTCCTGGGGGGGATATGATGAGCCTATTAA
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Kinase Functions
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                                                                                                                                                                                                                                      Having
                                                                                                                                                                                                                                      Polypeptides
                                                                1672 AGCCTTCAGGAGCAGAAGCTTCACAGGCTGAGAGCTCAGA 1711
                                                                                                                                                                                                                                                                                                                                                                                                       Score 713.8; DB 4;
Pred. No. 7.2e-185;
                                        2780 AGCCTATTGAGTATGAATACATTCATTCACAGGGCTCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                    APPLICANT: Marken, John S.
TITLE OF INVENTION: Human cDNAs Encoding I
FILE REFERENCE: 2877-US.
CURRENT APPLICATION NUMBER: US/09/509, 902A
CURRENT FILING DATE: 1999-08-03
NUMBER OF SEQ ID NOS: 16
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                                                                                                                                                                              Virca, Duke
Bird, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                          APPLICANT: Anderson, Dirk
                                                                                                                                                                                                                                                                                                       Patentin Ver.
                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens US-09-509-902A-6.
                                                                                                                                      Sequence 6, Application
Patent No. 6387676
                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
es 964; Conserv
                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                         RESULT 5
US-09-509-902A-6
                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                      ID NO 6
                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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SYSTEM: PC-DOS/MS-DOS PatentIn Release #1.0, Version #1.30

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-

Floppy disk

MEDIUM TYPE:

ZIP: 10036-2711 COMPUTER READABLE FORM:

New York

usa

COUNTRY:

US/09/442,100

DATA:

CURRENT APPLICATION DATA APPLICATION NUMBER:

SOFTWARE:

PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/411,111

CLASSIFICATION:

FILING DATE

FILING DATE: ATTORNEY/AGENT INFORMATION

(212) 790-9090 (212) 869-9741/8864

nucleic acid

TYPE: nucleic STRANDEDNESS:

unknown

MOLECULE TYPE:

TOPOLOGY:

NAME/KEY:

```
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6523
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-9741/8864
                                                                                                                                                                                                                                                                             TELEKAA 66141 PENNIE
TELEK: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 5720 base pairs
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1820 AGGACAACTIGTACTITGIGATGGACTACATTCCTGGGGGGATATGATGAGCCTATTAA 1879
                                             1880 TTAGAATGGGCATCTTTCCTGAAAATCTGGCACGATTCTACATAGCAGAACTTACCTGTG 1939
                                                                                             1940 CACTIGAAAGIGITCATAAAATGGGITTTATTCATAGAGATATTAAACCTGATAACATTT 1999
                                                                                                                                         2000 TGATTGACCGTGATGGCCATATTAAATTGACTGAĊTTTGGCTTGTGCACTGGCTTCAGAT 2059
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1354 AACAAGAAAGATGAAGAACGAAGAGTCTCGGATTCAGAGTTACTCCCCACAGGCCTTT 1413
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                                                                                                                                                          1414 AACTICTICATGGAGCAGCACGTAGAGAACGTCCTGAAGTCTCATCAGCAGCGTCTGCAT 1473
                                                                                                                                                                                                                 CGGAAGAAGCAGCTAGAAAATGAAATGATGCGGGTTGGATTATCTCAAGATGCCCAGGAT 1533
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                                                            Length 5720;
                                                                                     Indels
                                                         DB 4;
                                                        Score 521.2; DB 4;
Pred. No. 5.5e-132;
0; Mismatches 423;
                                                     16.2%;
                                                                                 Conservative
CDS
1103..4402
                                                                 Similarity
              LOCATION:
                                                  Query Match
Best Local Simi
Matches 852;
                       US-09-442-100-1
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NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS GENES AND METHODS BASED THEREON

Sequence 1, Application US/09442100 Patent No. 6359193 GENERAL INFORMATION:

US-09-442-100-1

APPLICANT: Xu, Tian APPLICANT: Tao, Wufan APPLICANT: Weng, Weiyi APPLICANT: Zhang, Sheng

APPLICANT:

E: Pennie & Edmonds 1155 Avenue of the Americas

ADDRESSEE: STREET: 11

NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS: APPLICANT: Yu, Wan TITLE OF INVENTION: TITLE OF INVENTION:

1;

Gaps

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us-09-763-334-3.rni

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1504 CGGGTTGGATTATCTCAAGATGCCCAGGATCAAATGAGAAAGATGCTTTGCCAGAAAGAG 1563
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    EXPRESSION
                                                                                                                                                                                                          Score 518.6; DB 4;
Pred. No. 8.3e-132;
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    GENES AND GENE
         FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 66, Application US/09328111 Patent No. 6262333
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  NOVEL HUMAN
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89.5%;
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                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                    TYPE: DNA
ORGANISM: HOMO
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Matches 570;
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                                                      3704 TCGAAGTACTACCAGGAGAACGGCAATCACTCGCGCCAGGACTCGATGGAGCCCTGGGAG
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                                                                                            TCCAAGTACTACC --- AGAGTGGGGATCACCCACGGCAAGATAGCATGGATTTCAGTAAC
                                                                                                                                                                                                                                                           GAATGGGGAGATCCTTCCAATTGTCGGTGTGGGGACAGACTGAAGCCACTGGAGCGGAGA
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                                      ATCTTTCCTGAAAATCTGGCACGATTCTACATAGCAGAACTTACCTGTGCAGTTGAAAGT
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Patent No. 6262333
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Bushnell, Steven E.
Carroll III, Eddie
Catino, Theodore J.
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Steinmann, Kathleen
Astle, Jon H.
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Lewis, Marcia E.
Monahan, John E.
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Bushnell, Steven E

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RESULT 9
US-08-878-989-11
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                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 678;
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                                                                                                        TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION TITLE OF INVENTION: PRODUCTS FILE REFERENCE: CCD-257 (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                   4.8e-93
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 376.6; D
Pred. No. 4.8e-
0; Mismatches
                                                                                                                          CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 678
                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-66
Carroll III, Eddie
Catino, Theodore J.
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match ' 11.7%;
Best Local Similarity 82.4%;
Matches 500; Conservative
                                                            Lewis, Marcia E.
Monahan, John E.
Schlegel, Robert
                                               Ford, Donna M.
                                Derti, Adnan
                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(678)
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match Best Local Similarity
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1414 AAGTICTICAIGGAGCAGCACGTAGAAGGICCIGAAGICTCAICAGCAGCGICIGCAI 1473
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                                                                                                                                                                                        DISEASE ASSOCIATED PROTEIN KINASES
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); Mismatches 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                  SEE: Incyte Pharmaceuticals, Inc
: 3174 Porter Drive
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/878,989
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Sequence 11, Application US/08878989
Patent No. 5885803
                                                     Bandman, Olga
Hillman, Jennifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
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                                                                                               Corley, Neil C.
Guegler, Karl G
                                                                                                                                 Lal, Preeti
Goli, Surya K.
Shah, Purvi
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NAME: Billings Incv T T
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LENGTH: 1935 base pair
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TELEX:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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CLONE: 705365
                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
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Best Local Similarity
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                           94304
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Incyte Pharmaceuticals, Inc. 3174 Porter Drive

ADDRESSEE:

STREET: STATE:

Palo Alto

COUNTRY:

Goli, Surya K. Shah, Purvi

SYSTEM: DOS FastSEQ for Windows Version

OPERATING SYSTEM:

SOFTWARE:

US/09/272,796

08/878,989

CLASSIFICATION:

FILING DATE

PF-0321 US

REFERENCE/DOCKET NUMBER:

TELEFAX: 415-845-4166

TELEX:

TELEPHONE:

NAME: Billings, Lucy J REGISTRATION NUMBER: 36

FILING DATE:

LENGTH: 1935 base pairs

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TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN TITLE OF INVENTION: KIRASES NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                              1894 TITCCIGAAAAICIGGCACGAIICIACAIAGCAGAACIIACCIGIGCAGIIGAAAGIGII 1953
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302 CTTGGCTTGGATGATTTTGAGTCTCTGAAAGTTATAGGAGGAGGAGCTTTTGGAGGGGG 361
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                                                                                            362 CGGTTGGTCCACAAAAAAGATACAGCCCATATCTATGCAATGAAGATGTTGAGAAAGTCT
                                                                                                                                                   GACGTTCTGCTCCGAAATCAGGTGGCTCATGTGAAAGCGGAGAGGGATATCCTAGCAGAA
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1414 AAGTTCTTCATGGAGCAGCACGTAGAGAACGTCCTGAAGTCTCATCAGCAGCGTCTGCAT 1473
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                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                       Score 248.4;
Pred. No. 8.3
                                                                                                                                                                                                                    7.7%;
ilarity 53.2%;
Conservative
nucleic acid
                                                                                                             LIBRARY: SYNORATO4
CLONE: 705365
                                                                                                                                                                                                                                              Best Local Similarity
Matches 599; Conserv
                                                                             IMMEDIATE SOURCE
                      STRANDEDNESS:
                                                                                                                                                                US-09-272-796-11
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Sequence 11, Application US/09272796 Patent No. 6207148

US-09-272-796-11

GENERAL INFORMATION:

Bandman, Olga Hillman, Jennifer Corley, Neil C. Guegler, Karl G.

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

CDS (596)..(1990)

; NAME/KEY: CI ; LOCATION: ( US-08-860-150-6

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                               TITCCTGAAAATCTGGCACGATTCTACATAGCAGAACTTACCTGTGCAGTTGAAAGTGTT
                                                                                    819 ACTICICATITICAGAACAIGAACTICAAAGAGGAAAGCAGAAACTIGGAAGAAGA-----
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RESULT 11
US-08-860-150-6
Sequence 6, Application US/08860150B
Patent No. 5991205
GENERAL INFORMATION:
APPLICANT: Hemmings, Brian A.
APPLICANT: Homes A.
TITLE OF INVENTION: Nuclear DBF2-Related (NDR) Kinases
FILE REFERENCE: 4.20265/APCT
CURRENT APPLICATION NUMBER: US/08/860,150B
EARLIER FILING DATE: 1997-06-19
EARLIER PLICATION NUMBER: PCT/EP95/05052
EARLIER PLICATION NUMBER: PCT/EP95/05052
SOFTWARE: PatentIn Ver. 1994-12-22
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 6
LENGTH: 3018
LENGTH: 3018
LENGTH: 3018
CERNOTH: 3018
CERNOTH: SORTHAND SAPIENS
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Length 3018;
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               3e-56;
              pred. No. 1.3e
0; Mismatches
     Score 244.4;
      7.68;
               53.48;
                Best Local Similarity 53.4 Matches 608; Conservative
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APPLICANT: Hemmings, Brian A.
APPLICANT: Milhward, Thomas A.
TITLE OF INVENTION: Nuclear DBF2-Related (NDR) Kinases
FILE REFERENCE: 14-20265/A/PCT
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Pred. No. 1.3e-56;
0; Mismatches 491;
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CURRENT FILING DATE: 1999-06-22
EARLIER APPLICATION NUMBER: 08/860,150
EARLIER FILING DATE: 1997-06-19
EARLIER APPLICATION NUMBER: PCT/EP95/05052
EARLIER APPLICATION NUMBER: PCT/EP95/05052
EARLIER FILING DATE: 1995-12-20
EARLIER FILING DATE: 1994-12-22
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VET: 2.0
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Patent No. 6040164
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Best Local Similarity 53.4%;
Matches 60%; Conservative
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; LOCATION: (596)..(1990)
US-09-338-132-6
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1898 CTGAAAATCTGGCACGATTCTACATAGCAGAACTTACCTGTGCAGTTGAAAGTGTTCATA 1957
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                                           1149 CAGAAGAGGAGACTCAGTTTTATATATAGCAGAAACAGTATTAGCCATAGACTCTATTCACC
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APPLICANT: Hemmings, Brian A.
APPLICANT: Hemmings, Brian A.
TITLE OF INVENTION: NUCLEAR DEB2-Related (NDR) Kinases.
FILE REFERENCE: 4-20265/A/PCT
CURRENT APPLICATION NUMBER: US/08/860,150B
CURRENT FILING DATE: 1997-06-19
EARLIER APPLICATION NUMBER: PCT/EP95/05052
EARLIER FILING DATE: 1995-12-20
EARLIER FILING DATE: 1994-12-22
NUMBER OF SEQ ID NOS: 18
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                                     30;
         Length 2101;
                                     Indels
        Score 198.6; DB 2;
Pred. No. 3.4e-44;
); Mismatches 489;
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        6.2%;
llarity 51.5%;
Conservative
                      Similarity
                                   Matches 552;
        Query Match
                        Best Local
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Indels
                                                                                                                                                                                                                     APPLICANT: Millward, Thomas A.
TITLE OF INVENTION: Nuclear DBF2-Related (NDR) Kinases; FILE REPERENCE: 4-20265/APCT
CURRENT APPLICATION NUMBER: US/09/338,132
CURRENT FILING DATE: 1999-06-22
EARLIER PRILOGATION NUMBER: OB/860,150
EARLIER PILING DATE: 1997-06-19
EARLIER PRILOGATION NUMBER: PCT/EP95/05052
EARLIER APPLICATION NUMBER: 94810746.1
EARLIER APPLICATION NUMBER: 94810746.1
EARLIER FILING DATE: 1994-12-22
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.0
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Pred. No. 3.4e-
0; Mismatches
                                                                                                                                   Sequence 1, Application US/09338132
Patent No. 6040164
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ORGANISM: Drosophila melanogaster
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Best Local Similarity 51.5%;
Matches 552; Conservative
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; LOCATION: (132)..(1499)
US-09-338-132-1
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US-09-338-132-1
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Search completed: January 16, 2003, 21:56:16 Job time : 124.372 secs
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APPLICANT: Philippsen, Peter
TITLE OF INVENTION: Fungal Target Genes and Methods
FILE REFERENCE: PB/5-30908A
CURRENT APPLICATION NUMBER: US/09/588,256
CURRENT FILING DATE: 2000-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 179.8; DB 4;
Pred. No. 4.6e-39;
0; Mismatches 487;
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Patent No. 6291665
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Best Local Similarity 49.8%;
Matches 530; Conservative
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Wendland, Juergen
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Flavier, Albert
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NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Ve.
SEQ ID NO 1
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US-09-588-256-1
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CTATATTCGTCTTAAAAGGGCTAAAATGGACAAGTCTATGTTTGTAAAGATAAAGACATT 1628
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being prin and is derived by analysis of the total score distribution.

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ubpna/US10\_NEW\_PUB.seq

ona/US09\_NEW\_PUB.sec

ubpna/US08\_NEW\_PUB.

oubpna/US07\_NEW\_PUB.s

Published Applications NA: \*

Database :

## SUMMARIÈS

		- <b>d</b> p				
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
1	681	21.2	2043	. 6	US-09-836-392-2	Sequence 2, Appli
c 5	518.6	16.1	638	. 10,	US-09-879-536-26	Sequence 26; App]
3	376.6	11.7	678	10	US-09-879-536-66	Sequence 66, App]
4	371.8	11.6	929	δ	US-09-764-868-214	
S	247.6	7.7	1689	σ	US-09-938-842A-1861	Ĥ
9	244.4	7.6	3583	6	US-09-974-298-152	Æ
7	212.6	9.9	1452	6	US-09-938-842A-2402	Sequence 2402, Ap
89	184	5.7	1818.	10	US-09-771-161A-89	
đ	175.2	5.5	734	σ	US-09-764-868-196	
10	136.4	4.2	1416	6	US-09-938-842A-2503	. m
11	132.8	4.1	1244	10	US-09-771-161A-38	Æ,
12	132.8	4.1	1393	10	US-09-771-161A-37	
13	132	4.1	1735	6	US-09-764-868-58	Ø
14	130.2	4.1	1398	σ	US-09-938-842A-633	
15	117.4	3.7	2365	0	US-09-981-353-6	Sequence 6, Appli
16	115.8	3.6	2311	10	US-09-810-808-6	Sequence 6, Appli
17	115.8	3.6	2370	6	US-10-000-039-1	· Sequence 1, Appli
18	115.8	3.6	. 2370	10	US-09-969-347-214	Sequence 214, Apr
19	115.8	3.6	2370	10	US-09-880-107-3855	

Sequence 1, Appli	Sequence 1, Appli	Sequence 46, Appl	Seguence 3, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 1, Appli	Sequence 2043, Ap	Sequence 8122; Ap	Sequence 297, App	Sequence 293, App	Sequence 3691, Ap	Sequence 1, Appli	Sequence 217, App	Sequence 399, App	Sequence 20, Appl		Seguence 570, App	Sequence 2146, Ap	Sequence 7789, Ap	Sequence 168, App	Sequence 2340, Ap	Sequence 6230, Ap	Sequence 403, App	Sequence 3, Appli	
10 US-09-804-471A-1 12 US-10-028-946-3	12 US-10-028-946-1	10 US-09-771-161A-46	10 US-09-799-875-3	10 US-09-799-875-1	9 US-10-017-216-3	9 US-10-017-216-1	10 US-09-294-093B-2043	9 US-09-796-692-8122	10 US-09-801-368-297	10 US-09-864-864-293	10 US-09-880-107-3691	10 . US-09-971-845-1	9 US-09-764-868-217	10 US-09-801-368-399	12 US-10-071-751-20	9 US-09-954-531-141	9 US-09-954-531-570	10 US-09-880-107-2146	9 US-09-796-692-7789	9 US-09-974-298-168	10 US-09-880-107-2340	10 US-09-867-701-6230	10 US-09-801-368-403	10 US-09-749-956-3	
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113	113	112.8	111.4	111.4	109.8	109.8	109.2	109	109	109	107	105	103.8	100	97.2	96.4	96.4	96.4	96.2	96	95.4	94.2	06	8.68	•
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## ALIGNMENTS

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FITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypeptides FITLE OF INVENTION: Antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 681;
                                                                                                                         CURRENT APPLICATION NUMBER: US/09/836,392
CURRENT TLING DATE: 2001-04-18
PURDA APPLICATION NUMBER: PCT/US00/28066
PRIOR FILING DATE: 2000-10-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
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Application US/09836392
                                                                    LION: Antibodies : PT020P1
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                 20020173458A1
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US-09-836-392-2
                                                APPLICANT: Ruben et al
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Best Local Similarity
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1687 TATGCAACAAAGACTCTTCGAAAGAAGACGTTCTGCTCCGAAATCAGGTGGCTCATGTG 1746
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                                       1867 ATGAGCCTATTAATTAGAATGGGCATCTTTCCTGAAAATCTGGCACGATTCTACATAGCA
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1444 GTCCTGAAGTCTCATCAGCAGCGTCTGCATCGGAAGAAGCAGCTAGAAAATGAAATGATG 1503
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                      1475 TITCGATGCCCAAAGCCTTCAGGAGCAGAAGCTTCACAGGCTGAGAGCTCAGA 1527,
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APPLICANT: Ford, Donna M.

APPLICANT: Lewis, Marcia E.

APPLICANT: Monaham, John E.

APPLICANT: Monaham, John E.

APPLICANT: Schlegel, Robert

TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

TITLE OF INVENTION: PRODUCTS

FILE REFERENCE: COL-257 (US)

CURRENT APPLICATION NUMBER: US/09/879,536

CURRENT FILING DATE: 2001-09-21
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 518.6;
Pred. No. 4.6
                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/088,801
PRIOR FILING DATE: 1998-06-10
                                                                                                   Sequence 26, Application US/09879536
Patent No. US20020144298A1
                                                                                                                                                                                       Burgess, Christopher C
Bushnell, Steven E.
Carroll III, Eddie
Catino, Theodore J.
                                                                                                                                             APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen
APPLICANT: Astle, Jon H.
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ilarity 89.5%;
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Best Local Similarity
                                                                                                                               GENERAL INFORMATION:
                                                                                     US-09-879-536-26/C
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ORGANISM: Homo sapiens
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US-09-764-868-214
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                                                          1627 TTAGGAATAGGAGCGTTTGGTGAAGTCTGTCTAGCAAGAAAAGTCGATACTAAAAGCTTTG 1686
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1924 GCAGAACTTACCTGTGCAGTTGAAAGTG----TTCATAAAATGGGTTTTATTCATAGAGAT 1980
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APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
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                                                                                                                    2041 TTGTGCACTGGCTTCAGATGGACACATGACTCCAAGT 2077
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                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/088,801
PRIOR FILING DATE: 1998-06-10
SOFTWARR: DATE: 1908-10
                                                                                                                                                                                                                            Sequence 66, Application US/09879536 Patent No. US20020144298A1
                                                                                                                                                                                                                                                                                                                    Burgess, Christopher C.
Bushnell, Steven E.
Carroll III, Eddie
Catino, Theodore J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (1)...(678)
; OTHER INFORMATION: n = A,T,C or G
US-09-879-536-66
                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen
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Best Local Similarity 82.4%;
Matches 500; Conservative
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                                                                                                                                                                                                                                                                                                       Astle, Jon H.
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ORGANISM: Homo sapiens
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LOCATION: (1)...(678)
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1924 GCAGAACTTACCTGTG-CAGTTGAAAGTGTTCAT--AAAATGGGTTTTATTCATAGAGAT 1980
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                                                                                                                                                                                      1867 ATGAGCCTATTAATTAGAATGGGCATC-TTTCCTGAAAATCTGGCACGATTCTACAT--A 1923
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                                                                                            480 CCAGAACTTACCTGNGCCNGTTGAAAGTGGTCCTTAAAATGGGGTTTAATTCTTAGAGT
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                                                              TCTTTCCAGGACAAGGACAACTTGTACTTTGTGATGGACTACATTCCTGGGGGGGATATG
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APPLICANT: Rosen et al
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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Pred. No. 1.3e-82;
2; Mismatches 175;
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CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
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; OTHER INFORMATION: n equals a,t,g, or
US-09-764-868-214
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Best Local Similarity 73.5%;
Matches 497; Conservative
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343 AIGGGGGTIGAIGACTITGAACTGCTIAGCATCAITGGCCGGGGTGCTITCGGTGAGGTG 402
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US-09-974-298-152
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TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
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                                           GAAGCCGACAATGAGTGGGTGGTCCGCCTGTACTACTTTTCCAGGACAAGGACAACTTG 1830
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           ATCTȚTCCTGAAAATCTGGCACGATTCTACATAGCAGAACTTACCTGTGCAGTTGAAAGT
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Pred. No. 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 05 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR RPLICATION NUMBER: US 60/300,111
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 8379
                                                                                                                                                                                                                                                                                                                                                   Sequence 1861, Application US/09938842A Patent No. US20020160378A1 GENERAL INFORMATION:
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US-09-938-842A-1861
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les 624; Conservative
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-09-938-842A-1861
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LENGTH: 1689
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TGTCTÄGCAAGAAAGTCGATACTAAAGCTTTGTÄTGCAACAAGACTCTTCGAAAGAA 1713
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                                                                     GACGTTCTGCTCCGAAATCAGGTGGCTCATGTGAAAGCGGAGAGGGATATCCTAGCAGAA
                                                                                          AGAATTTGTAAAGAAAATCTACTGGAAGCGTATATGCAATGAAAAAGTTAAAGAAATCC
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SEQ ID NO 2402
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                                                                                                                                                                                                                              NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020156263A1 347975.11
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Sequence 152, Application US/09974298
Patent No. US20020156263A1
GENERAL INFORMATION:
APPLICAMT: Chen; Huei-Mei
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
                                                                                                                                                                                                                                                                                   Score 244.4; DB 9;
Pred. No. 1.4e-50;
0; Mismatches 491;
                                                                FILE REFERENCE: PA 0037 P
CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
PRIOR PLING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 194
SEQ ID NO 152
LENGTH: 3583
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Best Local Similarity 53.4%;
Matches 608; Conservative
                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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                                          A-AATAGACGTCAGCTAGCCTTCTCCACAGTAGGCACTCCTGACTACATTGCTCCTGAGG
                                                                                                                                                                               GTGAAATGTTGGTGGGACAACCTCCTTTCTTGGCACAAACCCCATTAGAAACACAAATGA
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                                                                                           TGCTACTGCGAACAGGATATACACAGCTGTGTGACTGGTGGAGGTGTTGGTGTTATTCTTT
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TITLE OF INVENTION: STRESS-REGULATED GENES OF
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
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Pred. No. 6.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR PRIOR PLING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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Best Local Similarity
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CCTTATGTCGGGAGAGAAAGTCTGGAAATATTTATGCCATGAAGAAGTTAAAGAAATCT 384
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                                                APPLICATION OF A 1.

APPLICATE LEVENATION: et al.

TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REPERENCE: 805.2020-2005.1

CURRENT APPLICATION NUMBER: 05/09/771,161A

CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 136776

PRIOR APPLICATION NUMBER: 136776

PRIOR PILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: 136776

PRIOR APPLICATION NUMBER: 136776

PRIOR FILING DATE: 2000-04-15

PRIOR FILING DATE: 2000-04-12
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.7%; Score 184; DB 10;
Best Local Similarity 57.1%; Pred. No. 9.6e-36;
Matches 354; Conservative 0; Mismatches 265;
Sequence 89, Application US/09771161A Patent No. US20020110811A1 GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 89
                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-09-771-161A-89
                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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                               GENERAL INCORAGIONALIAN
GENERAL INCORMATION
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT23
CURRENT FILIA: DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 1510
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 196
LENGTH: 734
                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                            Score 175.2; DB 9;
Pred. No. 8.7e-34;
2; Mismatches 300;
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Sequence 196, Application US/09764868
Patent No. US20020168711A1
                                                                                                                                                                                                                                                                                                                                          Ouery Match 5.5%;
Best Local Similarity 54.8%;
Matches 410; Conservative
                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-868-196,
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TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 186;
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Pred. No. 5.5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: LEVINE, et al. TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR PAPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/227,866
  US/09938842A
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US-09-771-161A-38
US-09-771-161A-38
Sequence 38, Application US/09771161A
Patent No. US20020110811A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                         2001-08-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Arabidopsis thaliana
US-09-938-842A-2503
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Best Local Similarity 57.1%;
Matches 248; Conservative
                                                                                                                                                                                                               FILE REFERENCE: SCRIP1300-3
Sequence 2503, Application Patent No. US20020160378A1
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                                                                                                               APPLICANT: Wang, Xun APPLICANT: Zhu, Tong
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Length 139:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 58, Application US/09764868
Patent No. US20020168711A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PTZ32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 132; DB 9; Length 17
Pred. No. 7.6e-23;
2; Mismatches 182; Indels
                                                                            Score 132.8; DB 10;
pred. No. 4.2e-23;
0; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/764,868 CURRENT FILING DATE: 2001-01-17
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NUMBER OF SEQ ID NOS: 1510
SOFTWARE: Patentin Ver: 2.0
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Best Local Similarity 57.5%;
Matches 253; Conservative
                                                                                 ilarity 58.0%;
Conservative
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ORGANISM: Homo sapiens
US-09-764-868-58
; LENGTH: 1393
; TYPE: DNA
; ORGANISM: HOMO SapienS
US-09-771-161A-37
                                                                                     Ouery Match
Best Local Similarity
Matches 255; Conserv
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                                                                                                                                                                                                                                                                                                             Score 132.8; D. Pred. No. 4e-23
             FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
                                              CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR PELLING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
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PRIOR FILING DATE: 2000-04-12
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l Similarity 58.0%; P.
155; Conservative 0;
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PRIOR FILING DATE: 2000-06-15
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                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens US-09-771-161A-38
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255;

Best Local Matches 2

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Query Match

SEQ ID NO 38

SOFTWARE:

DNA

Length 1735;

PatentIn version 3.0

SOFTWARE:

NUMBER OF

US-09-771-161A-37

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COTHER INFORMATION: Incyte ID No. US20020160382A1 3819039CB1
US-09-981-353-6
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                                                                                                                                                                                                                       Mismatches
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CURRENT FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09981353 Patent No. US20020160382A1
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ilarity 56.5%;
Conservative
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APPLICANT: Lasek, Amy W.
APPLICANT: JONES, DAVID A.
TITLE OF INVENTION: GENES E
FILE REFERENCE: PA-0038 US
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Best Local Similarity
Matches 239; Conserv
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APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
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1729 AATCAGGTGGCTCATGTGAAAGCGGAGAGGGATATCCTAGCAGAAGCCGACAATGAGTGG 1788
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                                                                    1789 GTGGTCCGCCTGTACTACTCTTTCCAGGACAAGGACAACTTGTACTTTGTGATGGACTAC
                                                                                        477 ATCACCGCGCTGCACTACGCCTTTCAGGACGAGAACCACCTGTACTTAGTCATGGATTAC
                                  GCAGAGACCGCGTGCTTCCGAGAGGAGCGCGATGTGCTGGTGAACGGCGACTGCCAGTGG
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Pred. No. 1.9e-22;
0; Mismatches 203;
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PRIOR FILING DATE: 2000-08-24
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larity 55.4%;
Conservative
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APPLICANT: Harper, Jeff
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Matches 252; Conserv
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17.1 621 12 BG081236 15.8 694 10 AV708169 15.5 602 14 BQ201853 15.0 496 9 AL594372 14.6 473 9 AL594372 14.1 657 14 BM971435 14.0 475 12 BF740950 13.5 555 12 BF740950 13.1 930 14 BQ898648 13.1 930 14 BQ898648 13.1 637 9 AA910802 12.7 412 14 W75595	406         12.6         737         14         BM950668         BM950668           395.4         12.3         407         9         AA592233         AA592233           395.4         12.3         463         10         BE0603054         BE0603054           394.2         12.3         855         10         BE568367         BE568367           385.4         12.0         394         17         AZ503459         AA503459           369.2         11.5         559         10         AM642458         AM642458           359         11.2         68         13         B1331257         B1331257           350.6         10.9         863         10         BE620135         BE620135           349.6         10.9         863         17         AA216659         AA421650           345.6         10.6         405         10         BE093082         BE093082           340.4         10.6         405         10         BE093082         BE093082	339.6 10.6 957 14 BM601311 338.8 10.5 590 13 BM602863 338.8 10.5 590 13 BM6028663 335 10.4 581 12 BG143806 331.2 10.4 457 13 B1034906 331.2 10.3 579 13 B1034906 325.4 10.1 736 12 BG58495 318 9.9 824 13 B1225737 292 9.1 8774 13 BG958580 291.8 9.1 962 17 CNS0396F	RESULT 1 BB557112 LOCUS DEFINITION BB57112 RIKEN full-length enriched, 2 days pregnant adult female DEFINITION DEFINITION BB57112 C G::16448760 KEYWORDS SOURCE NOUSE mouse. ORGANISM WAS musculus C Chordata; Craniata; Vertebrata; Euteleostomi; REFERENCE 1, Chases 1 to 673; REFERENCE 1, Chases 1 to 673;	AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,  H. Hananoto,K., Hori,F., Ishii,Y., Ito,M., Kwahai,J., Konno,H., Kouda ,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki ,D., Shibata,K., Shinaqawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y. et al. 2001)  COMMENT On Aug 1, 2000 this sequence version replaced gi:9643478.  Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN)  1-7-22 Suehiro-Oho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
GenCorr ght (c) 1999 rch, using i 16, 2003, 03 3-334-3 cattcaattaac	Gapop 10.0 , Gapext 1.0  Searched: 16154066 seqs, 8097743376 residues  Total number of hits satisfying chosen parameters: 32308132  Minimum DB seq length: 0  Maximum DB seq length: 2000000000  Post-processing: Minimum Match 0%  Listing first 45 summaries	Database : EST:*  1: em_estba:* 2: em_esthum:* 3: em_estin:* 4: em_estin:* 5: em_estov:* 6: em_estpi:* 7: em_estpi:* 10: qb_esti:* 11: qb_htc:* 12: qb_esti:* 13: qb_esti:* 14: qb_esti:* 14: qb_esti:* 15: qb_esti:* 16: qb_esti:* 16: qb_esti:* 17: qb_esti:* 18: qb_esti:* 18: qb_esti:*	15: em_estiu:*  16: em_estom:*  17: eqss.lum:*  18: em_gss.lum:*  20: em_gss_lnv:*  21: em_gss_vrt:*  22: em_gss_vrt:*  24: em_gss_lun:*  25: em_gss_lun:*  26: em_gss_lun:*  27: em_gss_lun:*  26: em_gss_lun:*  27: em_gss_lun:*	4 1 Yd - 664191

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 665)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Dunn, D., Aoyagi, A., Barber, M., Meenen, E., Pedersen, T., Reilly Islam, H., Longarce, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., Muright, D., Weiss, R., Ander Maired and Varight, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb
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1M0072317F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0072317 F, DNA sequence
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                                308, Blomedical Polymers Research Bldg., 20 S. 2030
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Insert Length: 10000 Std Error: 0.00
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Seq primer: CGTTGTAAAACGACGGCCAGT
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                   RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) (2000) (2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 2000, 
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                                                                                                                                                                                               prepare full-length connection of the prepare full-length connection of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., watchiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matchiki, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
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Please visit our web site (http://genome.gsc.riken.go.jp/) for
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/dev_stage="2 days pregnant adult"
/lab_host="DH10B"
/lab_host="Site_1: SalI; Site_2: BamHI; cDNA library was
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory
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URL:http://genome.gsc.riken.go.jp,
Carningi,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., It
Carningi,P., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
M. Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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Computer-based methods for the mouse full-length cDNA
computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of
encyclopedia: real-time sequence clustering for construction of
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Ai
Kondo,S., Shinagawa,A., Itoh,M., Kawal,J., Shibata,K. and
Hayashisaki
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Pred. No. 2.1e-123;
0; Mismatches 1;
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cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Please visit our web site (http://genome.gsc.riken.go.jp/)
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                                                                                                                                                                                                                                                          (http://www.jax.org/resources/documents/dnares/). The DNA. was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor ollygonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance." 132\ c 204 g 167\ t
                                                                                                                                                                           /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-" /note="Vector: PWD42nv; Pulified genomic DNA from M. musculus C57BL/63 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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                                                                                                                                       /clone_lib="Mouse 10kb plasmid UUGC1M library"
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                                                          /organism="Mus musculus"
665.
                                                                           /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0072J17"
                    Location/Qualifiers
                                                                                                                                                            /sex="Male"
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BB174219 RIKEN full-length enriched, adult male hypothalamus Mus musculus cDNA clone A230050F21 3' similar to AF104414 Mus musculus large tumor suppressor 1 (Lats1) mRNA, mRNA sequence.
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer based methods for the mouse full-length cDNA
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Carnindi.P. Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carnindi.P., Shibatata,Y., Hayatsu,M. and Hayashizaki,Y.
No.malization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
perpare full-length cDNA libraries for rapid discovery of new
aggi.K., Fujiwake,S., 1000e,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
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The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
Tel: 81-45-509-922
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eŭkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 667).
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1028 CITTAGCCCCAACCCATCCTTCTTGGATGCCACGCCAGTTCAGACTGTTCAGCCTACCC
                                                                                                                                                                   ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
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On Jun 29, 2000 this sequence version replaced g1:8833302.
Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                           contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer \lceil 5^{\prime} \rceil
                                                                                                                                                                                               GAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTVN 3'], CDNA WAS
                                                                                                                                                       c Sciences Center and Genome Science Laboratory in Division of Experimental Animal Research in Riken
                                                                                                            /lab_host="DH10B"
/note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
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                                                       /clone_lib-"RIKEN full-length enriched, adult male
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Pred. No. 9.9e-114;
); Mismatches 17;
                                                                                        /tissue_type="hypothalamus"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                               156 t
                        /organism="Mus musculus"
                                  /db_xref="taxon:10090"
     Location/Qualifiers
                                            /clone="A230050F21"
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BI155504 648 bp mRNA linear EST 05-JUL-2001 602903902F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5033425 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs_r@mail.nin.gov
Classue Procurement::Lothar Hennighausen Ph.D., Chu-xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov d column: 02
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 648)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Pred. No. 4.7e-112;
0; Mismatches 1;
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/db_xref="taxon:10090"
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/lab_host="DH10B"
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Local Similarity 99.5%;
es 637; Conservative (
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                             2002
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             488
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Glibert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                         368
                                                                                                                                                                                                                                                                                                            548
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                   TTGAAAGTGTTCATAAAATGGGTTTTATTCATAGAGATATTAAACCTGATAACATTTTGA
                                                                                                                                                                                 TTGAAAGTGTTCATAAAATGGGTTTTAATTCATAGAGATATTAAACCTGATAACATTTTGA
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http://image.llnl.gov
Plate: LLAM11947 row: h column: 24
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Mammalia, Eutheria, Rodentia, Sciurognat
1 (bases 1 to 650)
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/tissue_type="tumor, biopsy
/dev_stage="5 months"
/lab_host="DH10B"
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quality sequence stop: 643.
    Location/Qualifiers
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Kargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K., Jaradat,S.A., Tanaka
,T.S., Carter,M.G. and Ko,M.S.H.
Verification and initial annotation of NIA mouse 15K cDNA clone set
Outpublished (2001).
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H3064C02-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
BG081357
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Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
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                                                                                                                                                     Length 650;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 600)
                                                                                                                                                                                             Indels
                                                                                                                                                  Score 567; DB 13;
Pred. No. 1.3e-102;
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95.4%;
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AUTHORS
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Large-scale cDNA analysis reveals phased gene expression
patterns during preimplantation mouse development, 2000,
Development, 127: 1737-1749; (3) Genome-wide mapping of
unselected transcripts from extraembryonic tissue of
7.5-day mouse embryos reveals enrichment in the t-complex, and under-representation on the x chromonal 1.5.
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                                                                                                                                                                                                                                                                                                                                                                                  /clone="H3064C02"
/clone_lib="NTA Mouse 15K cDNA Clone Set"
/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
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                                                                                    Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community.
visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
Plate: H3064 row: C column: 02
Seq primer: -21M13 Reverse
High quality sequence stop: 600
POLYAANO.
Contact: George J. Kargul
Laboratory of Genetics
Mational Institutes on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
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Pred. No. 7.7e-99;
); Mismatches 5;
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/db_xref="niaEST:H3064C02-5"
/db_xref="taxon:10090"
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    .600
    /organism="Mus musculus"

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Best Local Similarity 99.1%;
Matches 551; Conservative
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Contract: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
333 cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
mail: cdnadigaun.grc.nla.nih.gov
This clone set has been freely distributed to the community. Please
Visit http://dsun.grc.nla.nih.gov/cDNA/15k.html for details.
Plate: H3062 row: G column: 12
Seq primer: -21M13 Reverse
High quality sequence stop: 621
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//lab_host="Vector: pspORT1; Site_1: Sal1; Site_2: NotI; This fonce="Vector: pspORT1; Site_1: Sal1; Site_2: NotI; This calno is among a rearrayed set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 621)

*Rargul,6.J., Dudekula,D.B., Qian,Y., Lim,M.K., Jaradat,S.A., Tanaka,T.S., Carter,M.G. and Ko,M.S.H.
Unpublished (2001)
Other ESTS: H3062612-3
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety.of cDNA
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NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
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/strain="C57BL/6J"
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H3062G12 5', mRNA sequence.
BG081236
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1 (bases I to 694)

Pengy, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, Homo saplens cDNA ADC clones

Unpublished (2000)

Contact: Zequang Han

Contact: Zequang Han

Contact: Zequang Han

Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
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unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-comple and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
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AV708169 ADC Homo sapiens CDNA clone ADCALE11 5', mRNA sequence.
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                                                                               17.1%; Score 548; DB 12; 99.1%; Pred. No. 7.6e-99;
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Pred. No. 5.7e-91;
0; Mismatches 102; I
                                                                                        Shanghai
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                                                                                                                                                                                                                                                                                                         /note="Vector: pBluescript
201203, P. R. China
TTE1: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzq@chgc.sh.cn
This clone is available at CHGC in
                                                                                                                                                                                                                                                                                                                                                  162
                                                                                                                              1. .694
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ADCALE11"
/clone_lib="ADC"
                                                                                                                                                                                                                                        /tissue_type="Adrenal
/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                            Location/Qualifiers
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85.0%;
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Matches 591, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Facilitate Gene Discovery. Genome Research 6: 791-806, 1996.) The oligonucleotide used to prime first strand synthesis contained the sequence tag CACGTGAGAT between the Not I cloning site and d718 stretch. The rat cell line R3327-5P was provided by Mary Hendrix of the University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence contained an oligo-dy track that was present in the oligouclectie that was used to prime the synthesis of first coligouclectie that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NoIs site and the oligo-dy track served to verify it as a clone from the normalized rat cell line R3327-5p library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
          BQ201853 602 bp mRNA linear EST 02-MAY-2002 UI-R-DO1-cml-b-11-0-UI.sl UI-R-DO1 Rattus norvegicus cDNA clone UI-R-DO1-cml-b-11-0-UI 3', mRNA sequence.
                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2573 ACATCCCTAAAATCACGCATCCAACAGATACATCCAATTTCGACCCTGTTGATCCTGATA 2632
                                                                                                                                                                                                                                                                                                                                                                                                              451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT/T3D-Pac (Pharmacia) with a modified
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                                                                                                                                                                                                                                                      Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches to facilitate
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Pred. No. 9.8e-89;
0; Mismatches 53;
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JOWAL
TAG_TISSUB-rat cell line R3327-5p
TAG_SEQ=CACGTGAGAT"
120 c 108 g 198 t
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/strain="Sprague_Dawley"
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/clone="UT-R-DO1-CM1"b-11-0-UI"
/clone_lib="UT-R-DO1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l. 602
/organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                         Genome Res. 6 (9), 791-806 (1996)
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POLYA=Yes.
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                                                                                                                                                                                                                                           (bases 1 to 602)
                                                                                                                                                                                                                                                                                                                                                                                                          University of Iowa
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC5-BT0744-260 400-031-605kf3=2000-04-26&t4=1)
Seq primer: puc 18 forwart: 12
High quality sequence start: 12
High quality sequence stop: 467.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 578)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Magai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costar, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,

Brunstein, A., deOlivelra, P.S., Bucher, P., Jongeneel, C.V., O'Hare,

M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \operatorname{Simpson}, A . J . Shotgun sequencing of the human transcriptome with \operatorname{ORF} expressed
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                                  122 TGTACAATATTTTATTTTCCTAAGTTATGGGAAATGTTTTAAAATGTTATATTATTCCA
                                                                                                               AAAATGGGAAGCACCCCGAGCACGCTTTCTATGAGTTCACCTTTCGGAGGTTTTTTGATG
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20202663
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BE093083.1 GI:8483535
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Fax: +55-11-2707001
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                                          /note="Organ: breast; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ONESTES PCR (U.S. Letters Patent application No. 196 ,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue many and cDNA amplification were performed under low
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Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                            DB 10; Length 578;
                                                                                                                          1 others
                                                                                                                                                                                  Indels
                                                                                                                                                                                  47;
                                                                                                                                                          15.1%; Score 486.4; DB 1 91.6%; Pred. No. 1.4e-86;
                                                                                                                         165 t
                                                                                                                                                                                 0; Mismatches
                                                                                                             stringency conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
Rodentia;
                     /clone_lib="BT0744"
                               /dev_stage="Adult"
/organism="Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2431
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AI594372.1 GI:4603420
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1 (bases 1 to 496)
                                                                                                                                                                                  Conservative
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Wylie,T.,
v., Person
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                   Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            read is a RESEQUENCE of a previously sequenced mouse clone read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1701 TCTTCGAAAGAAAGACGTTCTGCTCCGAAATCAGGTGGCTCATGTGAAAGCGGAGAGGGGA 1760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATCCTAGCAGAAGCCGACAATGAGTGGGTGGTCGCCTGTACTACTCTTTCCAGGACAA 1820
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                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 TATCCTAGCAGAAGCCGACAATGAGTGGGTGGTCCGCCTGTACTACTCTTTCCAGGACAA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72
                                                                                                                                                                                                                                     Mashington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
TTE1: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 TGTTCGAAAGAAGACGTTCTGCTCCGAAATCAGGTGGCTCATGTGAAAGCGGAGAGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGACAACTTGTACTTTGTGATGGACTACATTCCTGGGGGGGATATGATGACGACCTATTAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Barstead mouse myotubes MPLRB5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 others
                                                                                                                                                    The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 481.4; DB 9;
Pred. No. 1.4e-85;
0; Mismatches 2;
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characteristic muscle proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer: -40RP from Gibco quality sequence stop: 472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="IMAGE:1049993"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_line="C2C12"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                           MGI:581569
This read is a RESEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
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llarity 99.6%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 correct orientation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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574

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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infociange.lini.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
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lungualished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/deb_host="Develor"
/note_host="pr73D-pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand
                                                                                                                                                                                                                                                                                        A1430221 473 bp mRNA linear EST 15-MAR me57h09.yl Soares mouse embryo NDME13.5 14.5 Mus musculus CDNA
                                                                                                                                                                                                                  ATCTCCCCTGTTCCACCTGGGGGGGGGGGGGGGTACCCTCCACCACCTCTTACCACT 420
                                                                                                                                              301 TGGGAACCAAGCTCTCAGACAAAGCGCTACTCTGGGAACATGGAGTACGTAATCTCCCGA.360
                                                                                                                                                               Confeact: Marra M/Washu-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                       CCACCACCTCCGAGAGGCCAGCCCACCTCCCCGAGGCACCACTCCCCCTCCCCCTCA
CCAAGCAATGGACAGAGAGTGAACCCCCCACCACCACCTCAAGTTAGGAGTGTTACTCCT
                   embryo NbME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="IMAGE:391649"
/clone_lib="Soares mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: -40RP from Gibco
High quality sequence stop: 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone IMAGE:391649 5',
A1430221
A1430221.1 GI:4276057
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                                                                                                                                                                                                                                                                                                                                                                            481 CAACCCATCATCAT 494
                                                                                                                                                                                                                                                                                                                                                                                                                 635 CTACCCTCCACCAT 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT. 13
AI430221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
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                                                    332
                 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                     658 bp mRNA linear EST 26-JAN-2001 ut60g11.y1 Soares_mouse_NMGB bcell Mus musculus cDNA clone IMAGE:332540 5' similar to TR:095835 095835 LARGE TUMOR SUPPRESSOR 1.; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 658)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.aih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1076704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 CAGGCGGATGTAGGAAGACCTCTGTCTGGATCCGGCATTGCAGCÁTTTGCTCAAGGTCAC 180
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                                                                            2121 CAGTAACGAATGGGGAGATCCTTCCAATTGTCGGTGTGGGGACAGACTGAAGGCCACTGGA 2180
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                                                                                               1 GTGCAACATTCAATTAACCGAAAACAAAGCTGGAAAGGTTCTAAAAGAGTCTCTAGTTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 658;
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/organism="Mus musculus"
/db_xxef="texon:10090"
/clone="IMAGE:332540"
/clone="IMAGE:332540"
/lab_host="DH10B (page-resistant)"
/lab_host="DH10B (page-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
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pred. No. 1e-84;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 473. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seg primer: -40RP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                  BG088986.1 GI:12571583
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97.8%;
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Best Local Similarity
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||GCGG ||496
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FEATURES

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

JOURNAL

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AI596344 458 bp mRNA linear EST 21-APR-1999 me57h09.x1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:391649 3' similar to TR:Q24096 Q24096 LATS. [1]; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 458)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, F., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., The Materston, R. and Wilson, P. The Mashu-Ni, Mouse EST Project 1999
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                                                                                                                                                                                                                                                                                                                                                                                   AGTCTGATTTTATCGTGCACCAAAATGTCCCCACTGGTTCTGTGACTCGGCAGCCACCAC
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                                                                                                                                                                      Length 473;
                                                                                                                                                                                             Indels
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                                                                                                                                                                  Score 468.2; DB
Pred. No. 6e-83;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI596344.1 GI:4605392
                                                                                                                                                                  Query Match
Best Local Similarity 99.4%;
Matches 470; Conservative
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KEYWORDS
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ORGANISM
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JOURNAL
COMMENT
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AUTHORS
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T 3', on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2 ]; double-stranded chyRN was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified ppT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatina Bonaldo. 143 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
High quality sequence stop: 449.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 AAGAGTGCGGACAGTGGTGACTCTGGGGATAAAAGAAAAGAAACAGATTACAACTTCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 ATCACTGTTCGGAAAAACAAGAAGATGAAGAACGAAGAGAGTCTCGGATTCAGAGTTAC
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  Parkway, Box 8501, St. Louis, MO
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                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 455; DB 9;
Pred, No. 2.5e-80;
0; Mismatches 0;
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                                                                                                                                                                                                                                     1. .458 /organism="Mus musculus
                                                                                                                                                                                                                                                                               /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:391649"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.2%; Sconilarity 100.0%; Poc
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                      /sex="unknown"
4444 Forest Park P
Tel: 314 286 1800
Fax: 314 286 1810
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Search completed: January 16, 2003, 21:48:49 Job time: 2795.39 secs
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                          EST 21-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (Tl phage resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue Procurement: Dr. M. J. Welsh, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: Lung; Vector: p17f13-Pac (Pharmacia).with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          following tissue(s): Primary Lung Epithelial Celis The library was constructed according to Bonaldo, Lennon and
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                  Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JI-CF-DU1 is a normalized cDNA library containing the
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                          M971435 657 bp mRNA linear EST 21-M7
I-CF-DU1-abd-1-16-0-UI.S2 UI-CF-DU1 Homo sapiens cDNA clone
I-CF-DU1-abd-1-16-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAG_LIB=UI-CF-DUI
TAG_TISSUB=Lung Epithelial Cells Tissue nos 359-368
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SEQUENCE: 1-30, NAT_ICH#LOW_COMPLEXITY
SEQUENCE: M13 FORWARD
POLYA*YES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    024 University of Iowa Med Labs, Iowa City, IA 52242, USA el: 319 356 4866
ax: 319 356 7171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="UI-CF-DU1-abd-1-16-0-UI".
/clone_lib="UI-CF-DU1".
/tissue_type="Primary Lung Epithelial Cells"
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                                                                                                                                                                                                                                                                                                                                                 Genome Res. 6 (9), 791-806 (1996)
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/db_xref="taxon:9606"
                        657 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  paul-mccray@uiowa.edu
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ilarity 82.5%;
Conservative
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Bonaldo, M.F.,
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Matches 520;
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ORIGIN
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TITLE
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

January 16, 2003, 09:50:52 ; Search time 5238:57 Seconds (without alignments) 17527.554 Million cell updates/sec Run on:

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## SUMMARIES

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## ALIGNMENTS

RESULT 1

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linear Xu,T., Tao,W., Wang,W., Zhang,S. and Yu,W. Nucleotide sequences of lats genes Patent: US 6359193-A 7 19-MAR-2002; Location/Qualifiers DNA Sequence 7 from patent US 6359193. AR201457 AR201457.1 GI:20252345 (bases 1 to 3155) Unclassified. Unknown. Unknown ACCESSION VERSION KEYWORDS SOURCE ORGANISM LOCUS DEFINITION REFERENCE AUTHORS TITLE JOURNAL FEATURES AR201457

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EGSAGPHPLDVDYGGSERRCPPPPYPKHLLLPSKSEQYSVDLDSLCTSVQQSLRGGTE
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HVENVIKTYQQKVSRRLQLEQEVAKAGLCEAEQEQMRKILYQKESNYNRLKRAKMDKS
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NEWVVKLYYSFQDKDSLYFVMDYIPGGDMMSLLIRMEVFPEHLARFYIAELTLAIESV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MRPKTFPATTYSGNSRQRLQEIREGLKQPSKASTQGLLVGPNSD"
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                                                                                                                                                                                                                                                                          Chordata, Craniata, Vertebrata, Euteleostomi,
Rodentià, Sclurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (22-FEB-1999) Hiroshi Nojima, Research Institute for
Microbial Diseases, Osaka University, Department of Molecular
Genetics; Yamadaoka 3-1, Suita, Osaka 565-0871, Japan
                                                                                                                                                                                                                                                                                                                     1 (sites)
Yabuta,N., Fujii,T., Copeland,N.G., Gilbert,D.J., Jenkins,N.P
Nishiguchi,H., Endo,Y., Toji,S., Tanaka,H., Nishimune,Y. and
                                                                                                                                                                                                                                                                                                                                                                                                               Structure, expression, and chromosome mapping of LATS2, a man homologue of the Drosophila tumor suppressor gene lats/warts Genomics 63 (2), 263-270 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (E-mail:hnojima@biken.osaka-u.ac.jp, Tel:81-6-6875-3980,
Fax:81-6-6875-5192)
                                                                                                                  bp mRNA linear RC
warts/lats-like kinase,
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/protein_id="BAA92380.1"
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· 3121 TTAGTACAGTATGGAAAGAGCACTTATTTGGGGG 3155
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Pred. No. 0;
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Location/Qualifiers
1. 3460
/organism="Mus musculus"
                                                                                                                                                                                                          MmLATS2; warts/lats-like kinase.
Mus musculus cDNA to mRNA.
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                                                                                                                                       musculus MmLATS2 mRNA
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Submitted (22-FEB-1999)
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/gene="MmLATS2"
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99.2%;
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	CTCCTGCCTTTTGCCAACGAGTCAGGCACTTCGGCAGCTGCAGAGGTGAACCGGCAGATG	CTTCAGGAGTTGGTGAATGCGGCATGTGACCAGGAGATGGCTGGC	ACGGGCAGTAGGAGTATCGAAGCTGCCTTGGAGTACATCAGTAAGATGGGCTACCTGGAC	CCCAGGAATGA	1 TCCACCCGGTGACTCGGCGGCCCAGTTTCGAGGGCACAGGGGAAGCACTCCCATCCTAC		TATTTAGACTTTCTC	CATCCTCCCAAAGGGTACAGCACAGCAGTAGAGCCAAGTGCGGCACTTTCCGGGCACACACA	1 TATGGTCGTGGTCATCTACTATCGGAGCAGTCTGGGTATGGGGTGCAGCGCAGTTCCTCTCTCT	1 TTCCAGAACAAGACGCCACCAGATGCCTATTCCAGCÁTGGCCAAGGCCCAGGTGGCCTTTTTTCTTCCAGCÁTGCCAAGGCCCAGGGTGGCCTTTTTTTTTT	1 CCGCCAGCCTCACCTTTCCTGCCCATGCT(	GCGGCTACCCCACCTGGGGCCCACCCATTÀCATGTGTTGGGCAC 	1 ACTGGCGAAAGCTCTGCACAGGCTGTGCTGGCACCGTCCAGGAACAGCCTCAATGCTGA 	TIGIACGAGCTGGGCTCCACGGTGCCCTGGTCTGCAGCTCCACTGGCACGCCGCGACTC	CTGCAGAAGCAGGGTCTAGAAGCCTCGCGGCGCATGTGGCTTTTCGGGCTGGCCCCAG	AGGACCAACTCCTTCAACAACCCACAACCTGAGCCCTCACTGCCGGCCCCCAACACGGT	1 ACCGCCGTGACGCCGCACACATCCTTCACCCTGTGAAGAGCGTGCGT	- G
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qa	Qy	Qy Db	Oy Db	Oy Dp	Oy Dp	Oy Op	. dg	Qy Db	oy do	Qy Dp	Oy Db	Oy Db	Q Q	oy do	oy Ob	Qy Dp	ço D	δλ

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2100 2419 2160 2539 1999 2040 2359 1560 1879 1620 1939 1680 1740 2059 1800 2119 1860 2179 1920 2239 1980 2299 1519 1320 1639 1380 1699 1440 1759 1500 1819 1200 1579 GAGCACCTGGCCCGCTTCTACATTGCAGAGTTGACCCTGGCCATTGAAAGTGTCCACAAG AAAGCTGGCAGAGACAAAAGAATTCAGACCTCCCGGTGCCTGTCCGCAAGAATAGC ATGGGCTTTATCCACCGGGACATCAAGCCTGACAACATACTCATCGACCTGGATGGTCAT ATTAAGCTGACAGATTTTGGCCTCTGCACTGGATTCAGGTGGACTCACAATTCCAAGTAC CTACAGCTGGAGCAGGAAATGGCCAAAGCTGGGCCTCTGTGAGGCCGAGCAGGAGCAGATG 1880 CTACAGCTGGAGCAGGAAGTGGCCAAAGCTGGGCTCTGTGAGGCCGAGCAGGAGAGGAGATG GCTTGTAAGCTGGACACTCACGCTCTGTACGCCATGAAGACTCTCAGGAAGAAGGATGTC CTGAACCGGAATCAAGTGGCCCATGTCAAGGCTGAGGGGACATCCTGGCTGAAGCAGAC AGTAAGTCTGAGCAGTACAGCGTGGACCTGGACAGCCTGTGCACCAGTGTGCAGCAGAGT CTGCGAGGGGGCACTGATCTAGACGGGAGTGACAAGAGCCACAAAGGTGCGAAGGGAGAC TICATGGAGCAACACGTGGAGAATGTCATCAAAACCTACCAGCAGAAGGTCAGCCGGAGG 1820 TICATGGAGCAACACGTGGAGAATGTCATCAAAACCTACCAGCAGAAGGTCAGCCGGAGG GCCACTGAGAGCCTGGAGACGAAGGAGGGCAGCCAGGCCCACACCCGCTGGATGTGGAC GCCACTGAGAGCCTGGAGAGGAAGGAGGCAGCACCACACCGCTGGATGTGGAC TATGGCGGCTCCGAGGCGCAGGTGCCCACCGCCTCCGTATCCAAAGCACTTGCTGCTGCCC 2480 2000 1741 2060 2120 1861 2180 2300 2041 2360 2101 2420 2161 1640 1700 1681 1801 1981 1400 1141. 1460 1520 1261 1580 1321 1381 1501 1561 1201 pp δy g γò g. ŏ pp Öλ á q q ζ g Ω, a ò g οý á ą ð ð g ζ X ž ą ð  $\stackrel{\sim}{\sim}$ ≿ ₹ ×  $\frac{7}{2}$ × Σ

Euteleostomi;

Homo sapiens

SOURCE ORGANISM

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PI JUNICHI KOGA,KEIKO KONO,ZOROTARYOFÜ FIODORU N PC
CI2N15/09,A61K31/00,A61K38/27,C07K14/47,C07K14/525,C12Q1/68, PC
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1. 5486
/organism='Homo sapiens (human)'.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6;
                                                                      Human tumor regulatory gene
Patent: JP 2000210086-A 1 02-AUG-2000;
NIHON CHEMICAL RESEARCH K K
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Pred. No. 0;
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PC A61K37/36,(C12N15/00,C12R1:91)
CC C Location/Qualif
FH Key Location/Qualif
FT Source 1. 5486
FT /Organism='Homo
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1. 5486
/organism="Homo sapiens"
/db_xref="1390 g 1266"
a 1452 c 1390 g 1266
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                                                                                                                           Homo sapiens (human)
JP 2000210086-A/1
02-AUG-2000
25-JAN-1999 JP 1999016223
                                  1 (bases 1 to 5486)
Koga,J., Kono,K. and N,Z.F.
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illarity 77.4%;
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5486 bp

E38226

RESULT E38226

Human tumor regulatory gene. E38226 E38226.1 GI:18626935 JP 2000210086-A/1.

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3 GGGGCACACTTCCCGCTGCAGGGCGCCGCACTACGGGCGGCCGCACCTGCTGGTGCCTGGG 1172	5 GAGCAGTCTGGGTATGGGGTGCAGCGGTTCCTCCTTCCAGAACAAGAGGCCACCAGAT 624   1	672			OCTGGGGCCCACCATTACATGTGTTGGGCACCCGGGGTCCCACGTTTACTGCCGAAAGC 792 	TCTGCACAGGCTGTGCTGGCACCGTCCAGGAACAGCCTCAATGCTGACTTGTACGAGCTG 852	GGCTCCACGTGCCTGGTGCGACCTCCACGTGGACCTGTATGATTG 14  GGCTCCACGTGCCTGGTCTGCAGCTCCACTGGCACGCCGCGACTGCTGCAG 90	AAGCAGGGTCTAGAAGCCTCGCGGCCGCATGTGGCTTTTCGGGCTGGC 954	CCCAGCAGGACCAACTCCTTCAACAACCCACAAC		GAGCCCTCCCTGCCCGCCCCCCAACGCGTGACGGCTGTCACGCCCGCGCAACTTGCAC 171	CCIGIGANGACCITCCITCTGCTGCGCCCGAGCCCCAGACAGCCGTGGGGCCCTCGCAC 1110	CCCGCCTGGGTGGCTGCGC		125	3 131.		) t) <u> </u>	GCCAAGGGGACAAAGGCGGAAAGGATAAAAAGCAGATTCAGACCTCTCCCGTTCCCGTC 2126	CGCAAGAATAGCAGAGATGAAGAGAAGAGAGAGTCTCGCATCAAGAGTTACTCCCCTTAT 1488 	154
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GTTCCTCCTTCCAGAACAAGACGCCACCAGAT 624 ACGTGCCGCACCACACCACAAGCAGGCCGGT 1352 CTGCCACCCTGGCCCGCGGGACTCCCTGCAG 1532 ACCAGCCGCGGCCCGGTCCGCCTGGCAAGGCC 1652 TIGGAGTACATCAGTAAGATGGGCTACCTGGAC 240 TTAAGCAGACCTCCCCAGGAAAGGCCTGGCG 300 ACTITCICITCCCTGGAGCCGGAGCCGGCACC 459 CCAAAGGGTACAGCACAGCAGTAGAGCCAAGT 519 ACTATGGTCGTGGTCATCTACT-----ATCG 564 066 998 TITLE TO THE TOTAL TO THE TOTAL GCCCAAGCTTCGGCGCTGACGGCCCAAGGCG 995 CTGCCTCGCACCACAAGCCGGCGGCTACCCCA 732 GCACCCGGGGTCCCACGTTTACTGGCGAAAGC 792 GGAACAGCCTCAATGCTGACTTGTACGAGCTG 852 CAGCTCCACTGGCACGCCGCGACTCGCTGCAG 906 SACCAGGAGATGGCTGGCAGAGCGCTCACGCAG 180 TCGAGGGCACAGGGGAAGCACTCCCATCCTAC 360 CCTCTGCAGCTGCAGAAGTGAACCGGCAAATG 695 CACAAC------CT CGCATGTGGCTTTTCGGGCTGGC------

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SKTPPPETGGYASLPTKGGGGPGGAGLAFPPPAAGLYVPHPHHKQAGPAHQLHYLGSR
SQVFASDSPPQSLLTPSRNSLNVDLYELSSTSVQQWPAATLARRDSLQKPGLEAPPRA
HVAFRPDCPVPSRTNSFNSHQPRPGBPGRAEPSLPAPNTVTAVTAAHILHPVKSYRVL
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PAPPEPDGKYVINWENTLH PROAVKLSBEARDLTAKLCCSADHRLGRWOADDLKAHPF
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GLMPTPVTRRPSFEGTGDSFASYHQLSGTPYEGPSFGADGPTALEEMPRPYVDYLFPG
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PDRRCPPPPYPKHLLLRSKSEQYDLDSLCAGMEQSLRAGPNEPEGGDKSRKSAKGDKG
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                                                                                     Hematology and Oncology, Kyoto University, Sakyoku, Kyoto, Kyoto Prefecture 606-8507,
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                                                                                                                                                                                                                                                                              /product="serine/threonine kinase
/protein_id="AAF80561.1"
/db_xref="G1:8886764"
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                                                                                                                                                                                                         /tissue_type="myeloid cell line" 375. .3641
                                                                                                                                                                                                                                               /note="similar to Drosophila
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llarity 77.3%; Pred. No. 0;
Conservative 0; Mismatches
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Submitted (20-NOV-1999)
54 Kawaracho, Shogoin, S.
Japan
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Yabuta,N., Fujii,T., Copeland,N.G., Gilbert,D.J., Jenkins,N.A
Nishiguchi,H., Endo,Y., Toji,S., Tanaka,H., Nishimune,Y. and
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HKMGFIHRDIKPDNILLIDLDGHIKLTPGELCTGFRWTHNSKYYQKGSHVRQDSMEPSD
                                           PFANESGTSAAAEVNRQMLQELVNAGCDQEMAGRALKQTGSRSIEAALEYISKMGYLD
PRNEQIVRVIKQTSPGKGLMPTPVTRRPSFEGTGDSFASYHQLSGTPYEGPSFGADGP
                                                                             VPGEPLGYGVQRSPSFQSKTPPETGGYASLPTKGOGGPPGAGLAFPPPAAGLVVPHPH
HKQAGPVAHQLHVLGSRSQVFASDSPPQSLLTPSRNSLNVDLYELSSTSVQQWPAATL
ARRDSLQKPGLEAPPRAHVAFRPDCPVPSRTNSFNSHQPRPGPPGKAEPSLPAPNTVT
                                                                                                                AVSAAHILHPVKSVRVLRPEPQTAVGPSHPAWVPAPAPAPAPAPAPAPAEGLDAKEEHA
LALGGAGAFPLDVEYGGPDRSARLRPTRSTCCCAKSEQYDLDSLCAGMEQSLRAGPNE
PEGGDKSRKSAKGDKGKDKKQIQTSPVPVRKNSRDEEKRESRIKSYSPYAFKFFMEQ
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VGVILFEMLVGQPPFLAPTPTETQLKVINWENTLHIPAQVKLSPEARDLITKLCCSAD
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                                 /translation="NSDTSLDAKVLGSKDATSSKQQMRATPKFGPYQKALREIRYSLL
                                                                   TALEEMPRPYVDYLFPGVGPHGPGHQHQHPPKGYGASVEAAGAHFPLQGAHYGRPHLL
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                                                                                       ACCTTCCGCAGGTTCTTCGATGACAACGGCTATCCCTTCCGGTGCCCGAAGCCCTCAG--
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X.T., Tao,W., Wang,W., Zhang,S. an
Nucleotide sequences of lats genes
Patent: US 6359193-A S 19-MAR-2002;
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St John, M.A., Tao, W. Fei, X., Fukumoto, R., Carcangiu, M.L.,
Brownstein, D.G., Parlow, A.F., McGrath, J. and Xu, T.
Mice deficient of Lats1 develop soft-tissue sarcomas, ovar
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Tao,W. and Xu,T.
Direct Submission
Submitted (04-NOV-1998) Genetics, HHMI, Yale University,
Congress Ave BCMM 254D, New Haven, CT 06536, USA
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Mus musculus large tumor suppressor 1 (Lats1) mRNA,
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Human homologue of the Drosophila melanogaster lats
suppressor modulates CDC2 activity
Nat. Genet. 21 (2), 177-181 (1999)
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/db_xref="taxon:10090"
/tissue_type="brain"
/dev_stage="newborn"
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TSLHIPPQAKLSPEASDLIIKLCRGFEDRLGKNGADBIKAHPFRYIDFSSDLRQQSA
SYPRXTHPPTOTSNFDPVDPOKLWSDGSEEBNISDTLSGWYKNGKHPBHAFYEFTFR
FYDDNGYPRYPKPFFFEYIHSGGSEGGSEGSDDOGHTSSDGNNRDLYYV"
1 764 c 696 g 807 L
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TLRKKDVLLTNQVAHVKAERDILAEADNEWVYRLYYSFQDKDNLYFVMDY IPGGDMMS
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TGFRWTHDSKYYQSGDHPRQDSMDFSNEWGDFSNCRCGDRLKFLERRAARQHQRCLAH
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                                                                                                                                                   /translation="VOHSINRKQSWKGSKESLVPQRHGPSLGENVVYRSESPNSQADV
GRPLSGSGIAAFAQAHPSNGGRVNPPPPPQVRSVTPPPPRGGTPPPRGTTPPPPSWE
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                                                            /note="putative serine threonine kinase; (MUM) Lats1"
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Pred. No. 5.5e-170;
0; Mismatches 644; Indels 18;
                                                                                                  =
                                                                                                    /product="large tumor suppressor
/protein_id="AAD16883.1".
.3213
/gene="Lats1"
<l. .2889</li>
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65.1%;
                                                      /gene="Lats1"
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Matches 1237; Conservative
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Pred. No. 2.7e-158;
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Nucleotide sequences of lats genes
Patent US 6359193-A 3 19-MAR-2002;
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Sequence 3 from patent US 6359193.
AR201455
AR201455.1 GI:20252343
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 4241)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human homolog of Drosophila warts tumor suppressor, h-warts, ocalized to mitotic apparatus and specifically phosphorylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nishiyama, Y., Hirota, T., Morisaki, T., Hara, T., Marumoto, T.,
Iida, S., Makino, K., Nakamura, H., Koga, H. and Saya, H.
Direct Submission
Submitted (30-JUN-1999) Tumor Genetics and Biology, Kumamoto
University School of Medicine, 2-2-1 Honjo, Kumamoto 860-0811,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to Drosophila warts tumor suppressor;
localized on mitotic apparatus, specifically
phosphorylated at mitotic checkpoint"
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Homo sapiens WARTS protein kinase (WARTS) mRNA, complete cds.
AF164041
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Nishiyama,Y., Hirota,T., Morisaki,T., Hara,T., Marumoto,T.,
Iida,S., Makino,K., Yamamoto,H., Hiraoka,T., Kitamura,N. and
                                                                                                       ATCAGCCACCCCATGGACACCTCCAATTTTGACCCGGTGGATGAAGAAAGCCCCTGGCAC
                                  TTCAACACCATCGACTTTTCCCGTGACATCCGAAAGCAGGCTGCACCCTACGTCCCCACC
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/protein_id="AAD50272.1"
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FEBS Lett. 459 (2), 159-165 (1999)
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SDAAKAEHNMSKMSTEDPRQVRNPPKFGTHHKALQEIRNSLLPFANETNSSRSTSEVN
                               PQMLQDLQAAGFDEDMVIQALQKTNNRSIEAAIEFISKMSYQDPRREQMAAAARPIN
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4307 bp mRNA linear PRI 18-MAR-1999 tumor suppressor 1 (LATS1) mRNA, complete cds.
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SDAAKAEHNMSKMSTEDPRQVRNPPKFGTHHKALQEIRNSLLPFANETNSSRSTSEVN
PQMLQDLQAAGFDEDMVIQALQKTNNRSIEAAIEFISKMSYQDPRREQMAAAARPIN
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                                                                                                           CATCCAGAGCACGCCTTCTATGAGTTCACCTTCCGCAGGTTCTTCGATGACAACGGCTAT
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St John, M.A., Tao, W., Fei, X., Fukumoto, R., Carcangiu, M.L.
Brownstein, D.G., Parlow, A.F., McGrath, J. and Xu, T.
Mice deficient of Latsl develop.soft-tissue sarcomas, ova
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Xu,T., Wang,W., Zhang,S., Stewart,R.A. and Yu,W. Identifying tumor suppressors in genetic mosaics: thlats gene encodes a putative protein kinase
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Human homologue of the Drosophila melanogaster lats
suppressor modulates CDC2 activity
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/protein_id="AAD16882.1"
/db_xref="GI:4324434"
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Nat. Genet. 21 (2), 182-186 (1999)
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Direct Submission
Submitted (04-NOV-1998) Genetics,
Congress Ave BCMM 254D, New Haven,
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/tissue_type="brain"
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1. .4307
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SSKFNFPSGRPGMONGTGQTDFMIHQNVVPAGTVNRQPPPPYPLTAANGOSPSALQTG GSAAPSSYTNGSIPQSMMVPNRNSHNMELXNISVPGLQTNWPQSSSAPAQSSPSSGHE IPTWQPNIPVRSNSFNNPLGNRASHSANSQPSATTVTAITPAPIQQPVKSMRVLKPEL

916 g 1337 BASE COUNT ORIGIN

Gaps 18; Length 4307; Indels Score 760; DB 9; I Pred. No. 2.8e-158; -0; Mismatches 665; 24.18; 63.78; Conservative Similarity Best Local Simi Matches 1197; Query Match

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2150 1224 CAACCTGAGCCCTCACTGCCCGCCCCCAACACGGTCACCGCCGTGACGGCCGCACACATC 1044 CTTCACCCTGTGAAGAGCGTGCGTGCTGCGGCCCCGAGCCCCAGACAGCCGTGGGGCCC 1104 2210 2330 1404 TCGCACCCCGCCTGGGTGGCTGCCCCACAGACCTGCCACTGAGAGCCTGGAGAGGAAG CCACCGCCTCCGTATCCAAAGCACTTGCTGCTGCCCAGTAAGTCTGAGCAGTACAGCGTG GAGGGCAGCCCACACCCGCTGGATGTGGACTATGGCGGCTCCGAGCGCAGGTGC GGAACCGCTTCAAATGTGACTGTGATGCCACCTGTTGCTGAAGCTCCAAACTATCAAGGA GACCTGGACAGCCTGTGCACTGTGCAGCAGAGTCTGCGAGGGGGCACTGATCTAGAC GGGAGTGACAAGAGCCACAAAGGTGCGAAGGGAGACAAAGCTGGCAGAGACAAAAAGCAG 985 1045 1105 2091 2031 1165 2151 1225 1285 1345 1405 2331 g ð g à à g ò g ò q g ò ò g ŏ

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Toshihiko,K., Shinichiro,T., Kyoko,N., Yasuyuki,N. and Hideyuki,S. warts Protein, polynucleotide encoding the protein, antisense polynucleotide thereof and antibody recognizing the protein Patent: JP 1999089580-4 1 06-APR-1999;
SUMITOMO ELECTRIC IND LTD
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JP 1999089580-A/1. unidentified. unidentified unidentified unclassified.
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PC (122N15/09,C07K14/435,C07K16/18,C1201/68,G01N33/53, P

COLON15/09,C12R1:91),(C12P21/02,C12R1:19),C12N15/00,

PC (C12N15/09,C12R1:91)

CC Strandedness: Double;

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                       CGCATCAAGAGTTACTCCCCTTATGCCTTCAAATTCTTCATGGAGCAACACGTGGAGAAT
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*** SEQUENCING IN PROGRESS ***
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Rattus norvegicus
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Nguyen, N. Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J.; Perez, L., Pickens, R., Primus, E., Pu, L., Oquiles, M., Ren'r., Rives, M., Rojas, A., Rojukokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Wang, S., Warden, C., Warlor, T., Washington, C., Watlington, S., Walliams, G., Williamson, A., Wleczyk, R., Wooden, S., Watlington, S., Wulliams, G., Williamson, A., Wleczyk, R., Wooden, S., Warley, K., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (23-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 17, 2002 this sequence version replaced gi:17941559.
Nguyen, A., Nguyen, N.
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Contact: hgsc-help@bcm.tmc.edu
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roshlikoo, R., Shinichiro,T., Kyoko,N., Yasuyuki,N. and Hideyuki,S.
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                                                                 CAACCTGAGCCCTCACTGCCCGCCCCCAACGGTCACCGCCGTGACGGCCGCGCGCACACATC
          506 CAGTAGAGCCAAGTGCGCACTTTCCGGGCACACTATGGTCGTGGTCATCTATCGG
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                                                                                    TASUVUKI NISHITANA, ALSHIMOLO, SHINICHIKU TAMBA, KYOKU NAGAMINE, PI TASUSTUKI SAYA,
PI HIDEYUKI SAYA,
PC CLANA, SOGO'RA14/435, CO7R16/18, C1201/68, G01N33/53, PC G01N33/532//C1201/09, C12R1:91), (C12P21/02, C12R1:19), C12N15/00, CC 12N15/09, PC G12R1:91), (C12P21/02, C12R1:19), C12N15/00, CC Strandedness: Double;
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT Source //organism='Unidentified'.
                                                                                                                                                                                                                                                                                                                                                                                                   TGTGAGGCCGAGCAGGAGCAGATGAGGAAGATCCTCTACCAGAAGGAGTCTAACTACAAC
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Patent: JP 1999089580-A 2 06-APR-1999;
SUMITOMO ELECTRIC IND LTD
OS Unidentified
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/organism="unidentified"
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Justice, R. W. Zilian, O., Woods, D.F., Noll, M. and Bryant, P.J.
The Drosophila tumor suppressor gene warts encodes a homolog of human myotonic dystrophy kinase and is required for the control Genes Dev. 9 (5), 534-546 (1995)
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tumor supressor (warts) mRNA exons 1-8,
Opoda; Hexapoda; Insecta; Pterygota,
Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                 TGGAGCGTCGGTGTGATTCTCTTTGAGATGCTGGTTGGGCAGCCGCCTTTCTTGGCCCC
                    GAGCCCGGTGACCTCTGGGACGATGTTTCCAACTGTCGCTGTGGAGACAGGTTAAAGACC
                                                                                          CTGGAGCAGAGGGCGCAGAAGCAGCACCAGAGGTGCCTGGCACATTCTCTTGTCGGGACA
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Drosophila melanogaster.
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Hexapoda;
Poeptera; Endopterygota; Diptera; Brachyce
Ephydroidea; Drosophilidae; brosophila.
1 (bases 1 to 5360)
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                                                                                                                           CTTCATGGAGCAACACGTGGAGAATGTCATCAAAACCTACCAGCAGAAGGTCAGCCGGAG
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                                           - AGAGATGAAGAGAGAGAGAGTCTCGCATCAAGAGTTACTCCCCTTATGCCTTCAAATT
                                                                GAAGGAGGAGGAGCGCAAGGAGTTCCGCATCAGGCAGTACTCGCCGCAAGCCTTCAAGTT
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/db_xref="taxon:7227"
/map="100A2-5"
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                                                                        2634 CCGARAGCAGCTGCACCTACGTCCCCACCATCAGCCACCCCATGGACACCTCCAATTT 2693
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--CTTTCCACGCTTTTTCGAATTTACCTT 4369
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Disease associated

Human Ndr serine/t Human NDR homologu

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Title: Perfect :

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Mouse; m-lats2 gene; large tumour suppressor; fetal brain; protein-serine/threonine-kinase; cell proliferation; antisense; dominant-negative; cancer; degenerative disorder; trauma; growth deficiency; therapy; antitumour; vulnerary; diagnostic; transgenic plant; transgenic animal; growth; senescence; ds.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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WPI; 1996-455275/45 P-PSDB; AAW06287 Wang senescence New 

This sequence encours a mouse tange towns curptocorn, and has been isolated from a newborn mouse brain phage lambda-ZAP cDNA library using a 2:2-kb DNA probe from the Drosophila lats gene: (AAT42117). A homologous mouse sequence has also been isolated (m-lats, AAT42119). The gene encodes a putative protein-serine/threonine-kinase, and inhibits cell proliferation and plays a strine/threonine-kinase, and inhibits cell proliferation and plays a strine/threonine-kinase, and inhibits cell proliferation and plays a function (e.g. an antisense objectuciocide or dominant-negative proliferative disorders, degenerative disorders, trauma, growth deficiency, etc., and fragments of the gene may be used as diagnostic probes. A lats-inhibitor sequence may be expressed in a transgenic plant or farm animal to confer increased growth and inhibit enhancing proliferation encodes a mouse large tumour suppressor m-lats2 gene for é Claim 8; Page 133-137; 215pp; English. isolated large tumour suppressor inhibiting cell proliferation or sedneuce

Sequence 3155 BP; 751 A; 924 C; 894 G; 586 T; 0 other;

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CTCCTGCCTTTTGCCAACGAGTCAGGCACTTCGGCAGCTGCAGAGGTGAACCGGCAGATG 120 180 240 240 300 Gaps 300 360 360 420 420 480 4.80 540 900 9 9 1 ATGAGAGCCACCCCGAAGTTTGGACCTTATCAAAAAGCTCTCAGGGAAATCCGATATTCC CCCAGGAATGAGCAGATTGTGCGAGTCATCAAGCAGACCTCCCCAGGAAAGGGCCTGGCG CCCAGGAATGAGCAGATTGTGCGAGTCATCAAGCAGAACCTCCCCAGGAAAGGGCCTTGGCG TCCACCCCGGTGACTCGGCGCCCAGTTTCGAGGGCACAGGGGAAGCACTCCCATCCTAC CATCCTCCCAAAGGGTACAGCACAGTAGAGCCAAGTGCGCACTTTCCGGGCACACAC TATGGTCGTGGTCATCTACTATCGGAGCAGTCTGGGTATGGGGTGCAGCGCAGGTTCCTCC CACCAGCTGGGTGGTGCAAACTACGAGGCCCCGCCGCACTGGAGGAGATGCCGCGGGAA DB 17; Length 3155; ; 0 Indels Score 3155; Pred. No. 0; 0; Mismatches ا. 0 100.0%; ilarity 100.0%; Conservative 0 Local Similarity Matches 3155; Query Match 61 61 121 121 181 241 181 241 301 301 361 361 421 421 481 481 541 ð g ò q ò g g ò à 셤 ò a ò g ò a ò g ò

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Mouse; Lats2; large tumour suppressor; cytostatic; vulnerary; cell overproliferation inhibitor; cdc2; cell cycle-dependent kinase; treatment; prevention; screening; cancer; skin; ovarian tumour; soft tissue sarcoma; pituitary disorder; gene therapy; hyperplasia; tit; luteinizing hormone hypogonadotropic hypogonadism; metaplasia; dysplasia; degenerative disorder; growth deficiency; physical trauma; hypoproliferative disorder; lesion; wound; lats knock-out mouse; ds.
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Use of lats proteins, complexes of lats and cdc2 for treating cancer that is refractory to treatment by standard chemotherapy and radiation therapy, and disorders associated with aberrant levels of cdc2 activity

English. Claim 44; Pages 112-117; 134pp;

The present sequence is a DNA encoding mouse lats2 (large tumour supressor) protein which is a cell overproliferation inhibitor and a supressor) protein which is a cell overproliferation inhibitor and supressors protein and cell cycle-dependent kinase odds/cyclin.A.

The present sequence is useful for treating cancer that is refractory to standard chemotherapy or radiation therapy such as hyperplasia, or disorders associated with aberrant netaplasia, or dysplasia, and disorders associated with aberrant level for disorders, promoting cdc2 function include degenerative disorders, growth deficiencies, hypoproliferative disorders, in which a lats gene has been disrupted by homologous preferably a mouse, in which a lats gene has been disrupted by homologous compunds that can be used to treat or prevent cancer, particularly compounds that the lats associated with pituitary dysfunction e.g. luteinizing hormone (IH) associated with pituitary dysfunction e.g. luteinizing hormone (IH) hypogonadotropic hypogonadism. The lats DNA is also used in gene therapy.

Sequence 3155 BP; 751 A; 924 C; 894 G; 586 T; 0 other;

ö Gaps DB 21; Length 3155; ; 0 Indels : 0 . k; Score 3155; D
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                                                                                                                                                                                                                                                                 s is the nucleotide sequence of a cDNA clone coding for a human hologue, i.e. hWART2 (see AAY06527), of Drosophila non-receptor ine/threonine kinase WART. hWART2 cDNA was isolated from a
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human bone marrow cDNA library using a PCR fragment of hWART1 as probe. hWART2 is consistently expressed in human tumour cells lines. exceptor mast of the colon cancer lines examined. This coverexpression in tumour cells versus normal tissues may provide a target for oncology drug development. Nucleic acids encoding full-length hWART2 and hWART2 polypeptides lacking one or more of full-length hWART2 and hWART2 polypeptides lacking one or more of a more of a main acid segments 1.33, 43-139, 43-466, 467-480, 514-518, and 974-1048, or lacking one or more of the N-terminal domain, catalytic domain, or C-terminal domain are claimed, as well as a hwart sequences (AAXR3396), hWART2 and hWART1 polypeptides, antibodies, a method for identifying madulators of hWART function, and use of such modulator compounds to treat an abnormal condition involving hWART signal transduction, especially cancer. Probes for 8\*666666666666888

Sequence 5276 BP; 1348 A; 1407 C; 1345 G; 1176 T; 0 other;

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CTCCTGCCTTTTGCCAACGAGTCAGGCACTTCGGCAGCTGCAGAGGTGAACCGGCAGATG 120 623 1160 683 360 Gaps 9 -----GGCCCCGCCGCA 399 ACCITICCTGCCCATGCTGGGCTGTACACTGCCTCGCACAAAGCCGGCGGCGGCTACCCCA 732 1 ATGAGAGCCACCCGAAGTTTGGACCTTATCAAAAAGCTCTCAGGGAAATCCGATATTCC ACGGGCAGTAGGAGTATCGAAGCTGCCTTGGAGTACATCAGTAAGATGGGCTACCTGGAC CCCAGGAATGAGCAGATTGTGCGAGTCATCAAGCAGACTCCCCCAGGAAAGGGCCTGGCG TCCACCCCGTGACTCGGCGGCCCAGTTTCGAGGGCACAGGGGAAGCACTCCCATCCTAC CTGGAGGAGATGCCGCGGGAATATTAGACTTTCTCTTCCCTGGAGCCGGAGCCGGCACC CACGGTGCCCAGGCTCACCAGCATCCTCCCAAAGGGTACAGGACACAGCAGTAGAGGCAAGT ------CACTTTCCGGGCACACTATGGTCGTGGTCATCTACT-----ATCG GAGCAGTCTGGGTATGGGGTGCAGCGCAGTTCCTTCCTCCAGAACAAAAAAGACGCCACCAGAT 1221 ACGGGGGTTACGCCAGCCTGCCCAGGGCCAGGGAGAGGCCCCAGGCGCCGCCTC GCC-----TATICCAGCATGGCC---AAGGCCCAGGGTGGCCCTCC---CGCCAGCCTC Indels DB 20; 544; Query Match
55.5%; Score 1749.6;
Best Local Similarity 77.4%; Pred. No. 0;
Matches 2389; Conservative 0; Mismatches Pred. No. 0; 0; Mismatches CACCAGCTGGTGGTGCAAACTACGAG-61 624 564 121 181 241 301 924 400 361 1161 984 460 520 265 625 1281 g ò g qq ò ò ò q ò g à q ô q ó q ò q ò g g ò ò qq ò 셤

1400 1520 1640 1050 1700 852 792 1191 1149 CTGCTGCCCAGTAAGTCTGAGCAGTACAGCGTGGACCTGGACAGCCTGTGCACCAGTGTG 1311 GAAGTGTGCCTCGCTTGTAAGCTGGACACTCACGCTCTGTACGCCATGAAGACTCTCAGG 1788 CCTGGGGCCCACCCATTACATGTTGGGCACCCGGGGTCCCACGTTTACTGGCGAAAGC TCTGCACAGGCTGTGCTGGCACCGTCCAGGAACAGCCTCAATGCTGACTTGTACGAGCTG GG-----CTCCACGGTGCCCTGGTCTGCAGCTCCÁCTGGCACGCCGCGACTCGCTGCAG CCTGTGAAGAGCGTGCGTGTGCTGCGGCCCGAGCCCCAGACAGCCGTGGGGCCCTCGCAC 1192 GATGTGGACTATGGGGGCTCCGAGGGGGGGGCCCCACGGCTCCGTATCCAAAGCACTTG GAGCCCTCACTGCCCGCCCCCAACACGGTCACCGCCGTGACGGCCGCACACATCCTTCAC --CCACAGCACCTGCCACTGAG ----GGGCAGCGCAGGCCCACACCCGCTG CAGCAGAGTCTGCGAGGGG----CACTGATCTAGACGGGAGTGACAAGGGCCACAAAGGT GCGAAGGGAGACAAAGCTGGCAGAGACAAAAAGCAGATTCAGACCTCCCCGGTGCCTGTC 2055 GCCAAGGGGGACAAAGGGGGAAAAGGATAAAAAGCAGATCAGACCTCTCCGGTTCCCGTC CGCAAGAATAGCAGAGATGAAGAAGAGAGAGTCTCGCATCAAGAGTTACTCCCCTTAT GCCTTCAAATTCTTCATGGAGCAACACGTGGAGAATGTCÀTCAAAACCTACCAGCAGAAG GTCAGCCGGAGGCTACAGCTGGAGCAGGAAATGGCCAAAAGCTGGGGCTCTGTGAGGCCGAG GCCAAGATGGACAAGTCCATGTTTGTGAAAATCAAGACTCTAGGCATCGGTGCCTTTGGG CAGGAGCAGATGAGGAAGATCCTCTACCAGAAGGAGTCTAACTACAACCGGCTGAAGAGG AAGCAGGGICTAGAAGCCTCGCGGC---CGCATGTGGCTTTTCGGGCTGGC CCCAGCAGACCAACTCCTTCAACAACCCACAAC CCCGCCTGGGTGGCTGCGC-1150 AGCCTGGAGACGAAGGA-1401 733 793 853 907 1521 1641 1051 1701 955 991 1111 1312 1369 1429 ( 1252 2115 1489 2175 1549 2235 1609 1669 2355 1729 Ω qq δ q δ g δλ g á Q δ g δ qq g ŏ Dp δ g ó qq qq δ , & Q g g ò

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a diagnostic pharmaceutical preparation for examining expression
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	3 2	ກ່ວ	TTGSACGCCCAAGGAGGAAGCATGCCCTGGCGCTGGGCGCGCGC
	Z Q	9 6	GATELGEACTATGGGGGGTCCGAGCGCACCGCCTCGGTATCCAAAGCACTTG 12 
	δŏ	L)	CTGCTGCCCAGTAAGTCTGAGCAGTAQAGGTAGAACTTGAAACTGTGTACAACTAGTGT 131
	QQ	1953	
	QY	1312	3CAGAGTCTGCGAGGGGGCACTGATCTAGACGGGAGTGACAAGAGCCACAAAGGT 136
	QQ	2007	CAGAGCCTCCGTGCGCCCCAACGAGCCCGAGGCGGCGACAAGAGCCCGAAAAGC 206
	Qy	1369	GCGAAGGGAGACAAAGCTGGCAGAGAAAAAGCAGATTCAGACCTCCCCGGTGCCTGTC 1428
	QΩ	2067	GGAAAGGATAAAAGCAGATTCAGACCTCTCCCGTTCCGTC 212
	δλ	4.2	CGCAAGAATAGCAGAGAGAAGAAGAGAGAGTCTCGCATCAAGAGTTACTCCCCTTAT 1488
	qq	2127	Capadacagcagaggaggaagaagagagagtcaggcatcagaggtagt
	δy	1489	CCTTCAAATTCTTCATGGAGCAACACGTGGAGAATGTCATCAAAACCTACCAGCAGAAG 154
	qq	2187	CTTTAAGTTCTTCATGGAGCAGCACGTGGAGAA
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	qq	2247	TAACCGGGGCTGCTGGGGCAGAAATGGC
	QY	9	CAGGAGCAGATGAGGAAGATCCTCTACCAGAAGGAGTCTAACTACAACCGGCTGAAGAGG 1668
	QQ	30	sgagcagatgcggaagatcctaccagaaagagtctaattacaacaggttaaagag
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. 0	Z d	487	AAAAAGGATGTCCTGAACCGGAATCAGGTGCCCCACGTCAAGGCCGAGAGGACATCTG 2546
*	Qy	1849	CTGAAGCAGACAATGAGTGGGTGGTCAAACTCTACTACTCCTTCCAGGACAAGGACAGC 190
	qq	2547	09
	QY	1909	STACTTTGTGATGGACTACATACCAGGCGGGATATGATGATGAGCCTGCTGATCAGGAT
	qq	2607	CTGTACTTTGTGATGGACTACATCCCTGGTGGGGACATGATGAGCCTGCTGATCCGGATG 2666
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The present sequence encodes a human growth hormone inhibited tumour suppressor (hGHITS) protein. The hGHITS proteins can be used in an antihnoplastic pharmaceutical preparation. Probes for the hGHITS DNA sequences can be used in diagnostic pharmaceutical preparations can be used for examining expression of hGHITS genes in dwarfism, gigantism, acromegaly, angiopathy, diabetic nephropathy or cardiopathy, or in mallignant cumours including breast cancer, renal adenocarcinoma, colorectal cancer, and leukaemia. Antibodies against the proteins can be used in a diagnostic pharmaceutical preparation for examining expression of
                                                                                                                                                                                                                                                                                                     New human growth hormone inhibited tumour suppressor genes 1 and 2 diagnosis of dwarfism, gigantism, acromegaly, angiopathy, diabetic nephropathy or cardiopathy
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          tumour; breast cancer;
antineoplastic; dwarfism; gigantism; acromegaly; angiop
diabetic nephropathy; cardiopathy; tumour; breast cance
renal adenocarcinoma; colorectal cancer; leukaemia; ss.
                                                                                                     /product= "tumour suppressor protein"
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Matches 2388; Conserv
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                     GTGATTCTCTTTTGAGATGCTGGTTGGGCAGCCGCCTTTCTTGGCCCCCCACCCCACAGAG
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          CTGGATGGTCATATTAAGCTGACAGATTTTGGCCTCTGCACTGGATTCAGGTGGACTCAC
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CACCAGCTGGGTGGAAACTACGAG	CTGGAGGAGATGCCGCGCGAATATTAGACTTTCTCTTCCCTGGAGCCGGAGCCGGCACC	CACGGGCCCAGGCTCACCAGCATCCTCCCAAAGGTACAGCACAGCAGTAGAGCCAAGT 	CGCACTITCCGGCACACACTATGGTCGTGGTCATCTACTATCG 	GACCACTGCGTATCGGGTGCAGCGCAGTTCCTCCTTCCAGAACAAGACGCCACCAGAT 	GCC:TATTCCAGCATGGCCAAGGCCCAGGGTGGCCCTCCCGCCAGCCTC	ACCTITCETGCCCATGCTGGGCTGTACACTGCCTCGACCACAAGCGGGGGGTACCCCACAAGCTTCCCACAAGCGGCGGGCTGTACGTGCCGGACCCACACCACAAGCAGGCGGGT	CTGGGGCCCACCCATTACATGTGTTGGGCACCGGGGTCCCACGTTTACTGGCGAAAGC	TCTGCACAGGCTGTGCTGGCACCGTCCAGGACAGCCTCAATGCTGACTTGTACGAGCTG	GGCTCCACGGTGCCCTGGTCTGCAGCTCCACGCCGCGCGCGACTCGCTGCAGAGACTCCGTGCAGGCACGCCGGGAGCTCCGAGAGAGA	AAGCAGGGTCTAGAAGCCTCGCGGCGCATGTGGCTTTTCGGGCTGGC	CCCAGCAGGACCAACTCCTTCAACAACCACAAC	GAGĆCCTCACTGCCCGCCCCCAACAGGTCACCGCGTGACGGCCGCACACCTTCAC 	CCTGTGAAGAGCGTGCGTGTGCTGCGGCCCGAGCCCCAGACAGCCGTGGGGCCCTCGCAC 	CCCGCTGGGTGGCTGCGC	AGCCTGGAGACGAAGGAGGGCAGCGCAGGCCCACACCCGCT	GATGTGGACTATGGCGGCTCCGAGCGCAGGTGCCCACCGCCTCCGTATCCAAAGCACTTG	CTGCTGCCCAGTAAGTCTGAGCAGTACAGCGTGGACCTGGACAGCTGTGCACCAGTGTG 
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у 361 b 936	у 400 b 996	y 460 b 1056	y 520 b 1113	y 565 b 1173	y 625 b 1233	y 673 b 1293	y 733 b 1353	y 793 b 1413	y 853 b 1473	у 907 b 1533	y 955 b 1593	y 991 b 1653	y 1051 b 1713	y 1111 o 1773	y 1150 o 1833	y 1192 5 1893	7 1252 3 1953
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GACATCCGAAAGCAGGCTGCACCCTACGTCCCCACCATCAGCCACCCCCATGGACACCTCC
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                                                                                                             marker;
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Pred. No. 0;
0; Mismatches 255;
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             AAZ61160 standard; cDNA; 1961
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llarity 84.4%;
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Local Similarity
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                                                                                                                                              Homo sapiens.
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Matches 1497;
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weight markers and as controls for peptide fragmentation

English.

1; Page 8-9; 60pp;

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                                                        CCTGGGCAGGATGGGGCAGATGACCTCAAGGCACACCCGTTCTTCAACACCATCGACTT 2621
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   CACAGAAACCCAGCTGAAGGTGATCAACTGGGAGAACACGCTCCACATTCCAGCCCAGGT
                                    GAGGCTCAGCGCTGAGGCCCGAGACCTCATCACGAAGCTGTGCTGCGCGGCTGACTGCCG
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peptide fragmentation control; cellular signal transduction; ss.
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/product= "kinase"
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New human kinase polypeptides and polynucleotides used as molecular

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a reagent to identify any proteins that the polypeptide regulates, and proteins with which it might interact. The polypeptides may also be used for preparation of antibodies. The antibodies can be used in assays to detect the presence of the protein, and to purify the protein
                                                                             The present sequence encodes a polypeptide which has kinase activity. The kinase polynucleotides can be used to express the polypeptides, and as probes to identify nucleic acids encoding proteins having kinase activity. The kinase polypeptides and fragmented polypeptides are used as molecular weight and isoelectric focusing markers, and as controls for peptide fragmentation. They also have a number of therapeutic uses as kinases play a central role in cellular signal transduction. The polypeptides could also be used as a reagent to identify any proteins. The polypeptides can also be used as a reagent to identify any proteins that the polypeptide regulates, and
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Pred. No. 3.5e-288;
0; Mismatches 196; Indels 9; G
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WO200155318-A2
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               Homo sapiens
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             718 AGACAGCCTGTACTTGTGATGGACTACATCCCTGGTGGGGACATGATGACGACTGCTGCTGAT
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                                                CAGGATGGAGGTCTTCCCTGAGCACCTGGCCCGCTTCTACATTGCAGAGTTGACCCTGGC
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2000US-0234997 2000US-0234998 New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives

Ruben SM;

Barash SC,

Rosen CA,

WPI; 2001-581633/65. P-PSDB; AAU87127.

(HUMA-) HUMAN GENOME SCI INC

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1-DEC-2000;
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The invention describes an isolated nucleic acid molecule (I) encoding a covel central nervous system protein. (I) and polypeptides (III) encoded cover cover control or treat a medical conditions and in diagnosis of a by (I), are used to treat a medical conditions and in diagnosis of a cutolmune diseases e.g. rheumatoid arthritis, hyperproliferative cutolmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. nervous system disorders e.g. Alzheimer's disease and amplobrophic lateral sclerosis, infections caused by bacteria, viruses c.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders c.g. orieral infection, gastrointestinal disorders e.g. disphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes disorders e.g. testicular feminisation, endocrine disorders e.g. cand pitutiary darfism, cancers and disorders at the cellular level e.g. coute kidney failure and blood related disorders e.g. myocardial cout from the polypeptides can also be used to aid wound healing and infarction. The polypeptides can also be used as a food additive or preservative to polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,
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Pred. No. 2.2e-280;
0; Mismatches 194; Indels 12; Gaps
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85.9%;
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Best Local Similarity 85.9
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AAD03989 standard; cDNA; RESULT 10
AAD03989
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neurodegenerative disorder; gastrointestinal disorder; cancer; lymphoma; blood coaqulation disorder; trauma; cerebrovascular disorder; tendonitis; gene therapy; nephrotic syndrome; glomerulonephritis; allergy; neoplasm; musculo-skeletal disorder; parkinson's disease; autoimmune disorder; behavioural disorder; renal disorder; ss.
                                                                      antifungal; antiparasitic; sarcoidosis; inflammation; asthma; arthritis; cardiovascular disorder; severe combined immunodeficiency; SCID; vaccine; hyperproliferative disorder; atherosclerosis; brain disorder; leukaemia; multiple sclerosis; Alzheimer's disease; vascular dementia; thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid molecule for producing human protein tyrosine
                                        Human protein tyrosine kinase receptor (PTK) cDNA from clone HMUBT71
                                                                                                                                                                                                                          "Human PTK protein from clone HMUBT71"
                                                             antibacterial;
                                                             tyrosine kinase receptor; PTK;
                                                                                                                                                                                           Location/Qualifiers
248..1585
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99US-0165914.
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                    (first entry)
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                                                             protein
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17-NOV-1999;
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                                                                                                                                                                          Homo sapiens
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                    02-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                       Ruben SM,
AAD03989;
                                                             Human;
                                                                                                                                                                                              Key
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The present cDNA sequence encodes human protein tyrosine kinase receptor (PTK) from clone HMTDB71.

(PTK) from clone HMTDB71.

The invention relates to human protein tyrosine kinase (PTK) receptors and their corresponding cDNA molecules. PTK receptors are useful in providing immunological probes for differential identification of the tissues or cell types present in a biological sample. PTK is used in methods for the diagnosis, prevention and treatment of various disorders immunodeficiency (SCID), inflammation); hyperpoinferative disorders (immunodeficiency (SCID), inflammation); hyperpoinferative disorders (neoplasm, sarcoidosis); cardiovascular disorders (multiple sclerosis), atherosclerosis); central nervous system disorders (multiple sclerosis), neurodegenerative disorders (Alzheimer's disease, Parkinson's disease); blood coaquiation disorders (Inflammatory disorders (asthma, called type); gastrointestinal disorders (inflammatory dosoders (asthma, called type); gastrointestinal disorders (inflammatory dosoders (asthma, called type); gastrointestinal disorders (inflammatory dosoders); health of carebrousesular disorders (inflammatory dosoders); disorders (uncomposed such as ovariam, concerts disorders (phenylketonuria); cancers (such as ovariam, concetts's disorders (phenylketonuria); cancers (such as ovariam, checkers); breast and lymphomas); behavioural disorders (roughorits); musculo-skeletal disorders (arthritis, trauma, tendonitis); renal disorders (nephrotic syndrome, glomerulonephritis); metastrases of malignancies and related disorders (leukaemia, multiple myeloma); and malignancies and related disorders (leukaemia, multiple myeloma); and "fortions caused by bacteria, viruses, fungi and parasities. PTK is also "fortions disease. PTK

Claim 1; Page 260-261; 288pp; English.

Sequence 2043 BP; 551 A; 528 C; 495 G; 469 T; 0 other;

nucleic acids are useful in gene therapy

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1585 AAAGCTGGGCTCTGTGAGGCCGAGCAGCAGCAGATGAGGAAGATCCTCTACCAGAAGGAG 1644
                                                                TCTAACTACAACCGGCTGAAGAGGGCCAAGATGGACAAGTCCATGTTTGTGAAATCAAG 1704
                                                                                                ACTCTAGGCATCGCTGCCTTTGGGGAAGTGTGCCTCGCTTGTAAGCTGGACACTCACGCT 1764
                                                                                                                                CTGTACGCCATGAAGACTCTCAGGAAGAAGGATGTCCTGAACGGGAATCAAGTGGCCCAT 1824
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                                        TACTCCTTCCAGGACAAGGACAGCCTGTACTTTGTGATGGACTACATACCAGGCGGGAT 1944
                                                                         ATGATGAGCCTGCTGATCAGGATGGAGGTCTTCCCTGAGCACCTGGCCCGCTTCTACATT 2004
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                     12;
                   188; Indels
 Score 1035.2; DB 2;
Pred. No. 1.1e-258;
0; Mismatches 188;
 32.8%;
85.4%;
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of cdc2 activity
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TTCAACACCATCGACTTTTCCCGTGACATCCGAAAGCAGGCTGCACCCTACGTCCCCACC
                 ATCAGCCACCCATGGACACCTCCAATTTTGACCCGGTGGATGAAGAAAGCCCCTGGCAC
                                                                                                                       CCAGAGCACGCCTTCTATGAGTTCACCTTCCGCAGGTTCTTCGATGACAACGGCTATCCC
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that is refractory to treatment by standard chemotherap
therapy, and disorders associated with aberrant levels
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Stewart RA;
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P-PSDB; AAY70391.
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lurenchalk GS,
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18-AUG-1998;
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δλ g qq Qγ a δy qq δλ qq ŏ q δy οp δ pp qq δλ g ò g δ g δ g ò qq ò g g δy g óλ δ ò ;; The present sequence is useful for treating cancer that is refractory to standard chemotherapy or radiation therapy such as hyperplasia, metaphasia, and disorders associated with aberrant levels of cdc2 activity. Conditions treated by promoting cdc2 function include degenerative disorders, growth deficiencies, hypoproliferative disorders, physical trauma, lesions, and wounds. An animal model preferably a mouse, in which a lats gene has been disrupted by homologous recombination, e.g. a lats knock-out mouse, is used for screening recompounds that can be used to treat or prevent cancer, particularly skin cancer, soft tissue sarcomas and ovarian tumours, and disorders associated with pituitary dysfunction e.g. luteinizing hormone (LH) hypogonadotropic hypogonadism. The lats DNA is also used in gene therapy. 1218 1404 1464 1443 1503 CGCATCAAGAGTTACTCCCCTTATGCCTTCAAATTCTTCATGGAGCAACACGTGGAGAAT 1524 1705 ACTCTAGGCATCGGTGCCTTTGGGGAAGTGTGCCTCGCTTGTAAGCTGGACACTCACGCT 1764 CAACCTGAGCCCTCACTGCCCGCCCCCAACACGTCACCGCCGCGCGTGACGGCCGCACATC 1044 CTTCACCCTGTGAAGAGCGTGCGTGCTGCGGCCCCGAGCCCCAGACAGCCGTGGGGCCC 1104 919 CACTCTGCTAATTCTCAGCCTTCTGCCACTACAGTCACTGCCATCACACCCGCTCCTATT 978 Gaps TCAGTAAGTAAGCCCTGCAAAGATGAACAGCCTAGCTTACCCAAGGAAGATGATAGTGAG TCTAACTACAACCGGCTGAAGAGGGCCCAAGATGGACAAGTCCATGTTTGTGAAAATCAAG TCGCACCCCGCCTGGGTGCCTGCGCCCACAGCACCTGCCACTGAGAGGACGAAG CCACCGCCTCCGTATCCAAAGCACTTGCTGCTGCCCAGTAAGTCTGAGCAGTACAGCGTG GACCTGGACACCTGTGCACCAGTGTGCAGAGTCTGCGAGGGGGCACTGATCTAGAC GGGAGTGACAAGAGCCACAAAGGTGCGAAGGGAGACAAAAGCTGGCAGAGACAAAAAGCAG GTCATCAAAACCTACCAGCAGAAGGTCAGCCGGAGGCTACAGCTGGAGCAGGAAATGGCC AAAGCTGGGCTCTGTGAGGCCGAGCAGGAGCAGATGAGGAAGATCCTCTACCAGAAGGAG CGGGTTGGATTATCTCAAGATGCCCAGGATCAAATGAGAAAGATGCTTTGCCAGAAAGAG GAGGGCAGCGCAGGCCCACACCCGCTGGATGTGGACTATGGCGGCTCCGAGCGCAGGTGC GGTACAGCTTCAAGTGTGCCTGTCATCCCACCTGTTGCTGAAGCTCCAAGCTATCAAGGT The present sequence is a DNA encoding mouse Lats (large tumour suppressor) protein which is a cell overproliferation inhibitor anegative regulator of cell cycle-dependent kinase cdc2/cyclin A. 18; Length 3213 Score 812.6; DB 21; Length Pred. No. 1.1e-200; 0; Mismatches 644; Indels Sequence 3213 BP; 946 A; 764 C; 696 G; 807 T; 0 other; Claim 44; Fig 13; 134pp; English Ouery Match 25.8%; Best Local Similarity 65.1%; Matches 1237; Conservative 1105 1165 1219 1585 985 1045 1099 1225 1324 979 1405 1465 1384 1525 1504 1645 1564 ð g ò g ò ద ò QO ö g οχ a δ Q ò 8 Q g ò g ò g ò g ô

2484 2604 2064 2124 2184 2223 2424 2403 2544 2463 2304 2364 CATCCAGAGCACGCCTTCTATGAGTTCACCTTCCGCAGGTTCTTCGATGACAACGGCTAT 2841 ||||| | ||| || || ||||||||||| || || ||| ||| ||| ||| || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || AAGCCTGACAACATCATCGACCTGGATGGTCATATTAAGCTGACAGATTTTGGCCTC TTGTATGCAACAAAGACTCTTCGAAAGAAAGACGTTCTGCTCCGAAATCAGGTGGCTCAT ATGATGAGCCTGCTGATCAGGATGGAGGTCTTCCCTGAGCACCTGGCCCGCTTCTACATT GCAGAGTTGACCCTGGCCATTGAAAGTGTCCACAAGATGGGCTTTATCCACCGGGACATC TGCACTGGATTCAGGTGGACTCACAATTCCAAGTACTACCAGAAAGGGAACCACATGAGA CTTGTCGGGACACCAAATTACATCGCTCCGGAGGTGCTTCTCCGCAAAGGGTACACGCAG CTCTGTGACTGGAGGCGTCGGTGTGATTCTCTTTGAGATGCTGGTTGGGCAGCCGCCT TTCTTGGCCCCCCACCCCCACAGAGGCGCAGCTGAAGGTGATCAACTGGGAGAGCACGCTG CATATCCCTACGCAGGTGAGGCTCAGCGCTGAGGCCCGAGACCTCATCACGAAGCTGTGC TGCGCGGCTGACTGCCGCCTGGGCAGGGATGGGGCAGATGACCTCAAGGCACACCCGTTC TTCAACACCATCGACTTTTCCCGTGACATCCGAAAGCAGGCTGCACCCTACGTCCCCACC ATCAGCCACCCCATGGACACCTCCAATTTTGACCCGGTGGATGAAGAAAGCCCCTGGCAC GAGGCCAGCGGAGAG---AGCGCCAAGGCCTGGGACACGCTGGCCTCCCCCAGCAAG TACTCCTTCCAGGACAAGGACAGCCTGTACTTTGTGATGGACTACATACCAGGCGGGAT CAGGACAGCATGGAGCCCGGTGACCTCTGGGACGATGTTTCCAACTGTCGCTGTGGAGAC AGGTTAAAGACCCTGGAGCAGAGGGCGCAGAAGCAGCACCAGAGGTGCCTGGCACATTCT = 1684 1885 1945 2065 2125 2044 2545 2524 2584 1624 1765 1744 1804 2005 1924 1984 2185 2104 2245 2164 2305 2365 2425 2344 2485 2404 2464 2605 2725 2644 2782 δ

M-lats

Key

RESULT 12

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                     2704 CACCCCGAGCACCCTTTCTATGAGTTCACCTTTCGGAGGTTTTTTGATGACAATGGCTAC 2763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enhancing proliferation
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                                                                                                                                                                                                                                                                                                                                       Mouse; m-lats gene; large tumour suppressor; fetal brain; protein-serine/threonine-kinase; cell proliferation; antisense; dominant-negative; cancer; degenerative disorder; trauma; dominant-negative; therapy; antitumour; vulnerary; diagnostic; transgenic plant; transgenic animal; growth; senescence; ds.
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Pred. No. 7.6e-200;
0; Mismatches 646;
                                                                                                                                                                                                                                                                                                             encoding large tumour suppressor.
                                                               2842 CCCTTCCGGTGCCCGAAGCCCTCAGAGCCCGCAGAGAGT
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for inhibiting cell proliferation or
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                                                                                                                            GAGGGCAGCGCAGGCCCACACCCGCTGGATGTGGACTATGGCGGCTCCGAGCGCAGGTGC 1224
                             979 CAACAGCCCGTGAAAAGCATGCGCGTCCTGAAACCAGAGCTGCAGGACTGCTTTAGCCCCA 1038
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dominant-negative; cancer; degenerative disorder; trauma;
growth deficiency; therapy; antitumour; vulnerary; diagnostic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; h-lats gene; large tumour suppressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H-lats gene encoding large tumour suppressor
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Location/Qualifiers

Key

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This sequence encodes a human large tumour suppressor h-lats protein, and has been isolated from a fetal human brain phage lambda-gt10 cDNA library using a 2.1-kb DNA probe from the mouse m-lats gene (AAT42119). The full-length cDNA is present in plasmid pBS(KS)-h-lats. The gene encodes a putative protein-serine/threonine-kinase, and inhibits cell proliferation and plays a crucial role throughout development. Activators or inhibitors of lats function (e.g. an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1833. GGAACCGCTTCAAATGTGACTGTGATGCCACCTGTTGCTGAAGCTCCAAACTATCAAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   degenerative disorders, trauma, growth deficiency, etc., and fragments of the gene may be used as diagnostic probes. A
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Pred. No. 6e-187;
0; Mismatches 665;
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63.78;
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P-PSDB; AAW05178.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; Lats; large tumour suppressor; cytostatic; vulnerary; cell overproliferation inhibitor; cdc2; cell cycle-dependent kinase; treatment; prevention; screening; cancer; skin; ovarian tumour; soft tissue sarcoma; pituitary disoncer; gene therapy; hyperplasia; bH; luteinizing hormone hypogonadotropic hypogonadism; metaplasia; dysplasia; degenerative disorder; growth deficiency; physical trauma; hypoproliferative disorder; lesion; wound; lats knock-out mouse; ds.
                         TGCGCGGCTGACTGCCGCCTGGGCAGGGATGGGCCAGATGACCTCAAGGCACACCCGTTC
3138 CACATTCCACCACAAGCTAAACTCAGTCCTGAAGCTTCTGATCTTATTATAAACTTTGC
                                        TTCAACACCATGGACTTTTCCCGTGACATCCGAAAGCAGGCTGCACCCTACGTCCCCACC
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Stewart RA;
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P-PSDB; AAY70390.
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1705 ð g δ g οy 염 δy g Qγ .g Dp δy Op d  $\mathop{\rm Qy}_{\cdot}$ δý Db à Dp δ g Dp Qγ qq δ Db δ Ω g δ qq ŏ δy ŏ q negative regulator of cell cycle-dependent kinase cdc2/cyclin A. The present sequence is useful for treating cancer that is refractory are standard chemotherapy or radiation therapy such as hyperplasia, metaplasia, and disorders associated with aberrant levels of cdc2 activity. Conditions treated by promoting cdc2 function include degenerative disorders, growth deficiencies, hypoproliferative disorders, physical trauma, lesions, and wounds. An animal model preferably a mouse, in which a lats gene has been disrupted by homologous recombination, e.g. a lats knock-out mouse, is used for screening compounds that can be used to treat or prevent cancer, particularly skin cancer, soft tissue sarcomas and ovarian tumours, and disorders associated with pituitary dysfunction e.g. luteinizing hormone (LH) hypogonadotropic hypogonadism. The lats DNA is also used in gene therapy. 1952 1832 1164 1404 2057 2117 1524 1584 1644 CAACCTGAGCCCTCACTGCCCGCCCCCAACACGGTCACGCCGTGACGGCCGCACACATC 1044 CTTCACCCTGTGAAGAGCGTGCGTGTGCTGCGGCCCGAGCCCCAGACAGCCGTGGGGCCC 1104 a The present sequence is a DNA encoding human Lats (large tumour suppressor) protein which is a cell overproliferation inhibitor and GGAACCGCTTCAAATGTGACTGTGATGCCACCTGTTGCTGAAGCTCCAAACTATCAAGGA ccaccaccaccacaaaacarcrecrecaaaaccarcrerrerrerrerre TCAATCAGTAAGCCTAGCAAAGAGGATCAGCCAAGCTTGCCCCAAGGAAGATGAGAGTGAA GGGAGTGACAAGAGCCACAAAGGTGCGAAGGGAGACAAAGCTGGCAGAGAAAAAGCAG CGCATCAAGAGTTACTCCCCTTATGCCTTCAAATTCTTCATGGAGCAACACGTGGAGAAT GTCATCAAAACCTACCAGCAGAAGGTCAGCCGGAGGCTACAGCTGGAGCAGGAAATGGCC **AAAGCTGGGCTCTGTGAGGCCGAGCAGGAGCAGATGAGGAAGATCCTCTACCAGAAGGAG** CGGGTTGGATTATCTCAAGATGCCCAGGATCAAATGAGAAAGATGCTTTGCCAAAAAGAA TCGCACCCCCCCCTGGGTGCCTGCGCCCCACTGCCCACTGAGAGCCTGGAGAAG ACACACCCTTCTTGGATACCACAGCCAATTCAAACTGTTCAACCCAGTCCTTTTCCTGAG GAGGGCAGCGCACACACCCGCTGGATGTGGACTATGGCGGCTCCGAGCGCAGGTGC CCACCGCCTCCGTATCCAAAGCACTTGCTGCTGCCCAGTAAGTCTGAGCAGTACAGCGTG GACCTGGACAGCCTGTGCACCAGTGTGCAGCAGAGTCTGCGAGGGGGCCACTGATCTAGAC CGTATTCAAAGTTATTCTCCTCAAGCATTTAAATTCTTTATGGAGCAACATGTAGAAAAT TCTAACTACAACCGGCTGAAGAGGGCCAAGATGGACAAGTCCATGTTTGTGAAAATCAAG DB 21; Length 3984; Indels Sequence 3984 BP; 1280 A; 847 C; 798 G; 1059 T; 0 other; 0; Mismatches 665; 24.1%; Score 760; DB 2; llarity 63.7%; Pred. No. 6e-187; Conservative 0; Mismatches 66 English Fig 12; 134pp; Best\_Local Similarity Matches 1197; Conserv AAGAGTTA Claim 44; Query Match 1773 1833 1285 2118 2178 1653 1045 1105 1225 1893 1345 2013 1405 2058 1465 2238 2298 985 1713 1165 1953 1585 1645

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2777 3077 2841 GCAGAGTTGACCCTGGCCATTGAAAGTGTCCACAAGATGGCCTTTATCCACGGGACATC 2064 2124 2837 2957 3017 2424 2484 3137 3197 2604 2781 3437 1884 1944 2597 2004 2184 2897 2304 2364 3257 2724 ACTCTAGGCATCGGTGCCTTTGGGGAAGTGTGCCTCGCTTGTAAGCTGGACACTCACGCT TACTCCTTCCAGGACAGGACAGCCTGTACTTTGTGATGGACTACATACCAGGCGGGGAT ATGATGAGCCTGCTGATCAGGATGGAGGTCTTCCCTGAGCACCTGGCCCGCTTCTACATT CTTGTCGGGACACCAAATTACATCGCTCCGGAGGTGCTTCTCCGCAAAGGGTACACGCAG TEGETEGGACTCCCAATTATATTGCACCTGAAGTGTTGCTACGAACAGGATACACACAG CTCTGTGACTGGGGGGGCGTCGGTGGTTCTTTTGAGATGCTGGGCGCGCCCT CACATTCCACCACAAGCTAAACTCAGTCCTGAAGCTTCTGATCTTATTAAAACTTTGC TGGGGGGTGACTGCCGCCTGGGCAGGGATGGGGCAGATGACCTCAAGGCACACCCGTTC ATCAGCCACCCCATGGACACCTCCAATTTTGACCCGGTGGATGAAGAAAGCCCCTGGCAC CATCCAGAGCACGCCTTCTATGAGTTCACCTTCCGCAGGTTCTTCGATGACAACGGCTAT CTGTACGCCATGAAGACTCTCAGGAAGAAGGATGTCCTGAACCGGAATCAAGTGGCCCAT **AAGCCTGACAACATACTCATCGACCTGGATGGTCATATTAAGCTGACAGATTTTGGCCTC** TGCACTGGATTCAGGTGGACTCACAATTCCAAGTACTACCAGAAAGGGAACCACATGAGA CAGGACAGCATGGAGCCCGGTGACCTCTGGGACGATGTTTCCAACTGTCGCTGTGGAGAC AGGTTAAAGACCCTGGAGCAGAGGGCGCAGAAGCAGCACCAGAGGTGCCTGGCACATTCT TTGTGTGATTGGTGGAGTGTTGGTGTTATTCTTTTTGAAATGTTGGTGGGACAACCTCCT TTCTTGGCCCCCCACCCCCACAGAGGAGGCTGAAGGTGATCAACTGGGAGAGCACGCTG CATATICCCTACGCAGGTGAGGCTCAGCGCTGAGGCCCGAGACCTCATCACGAAGCTGTGC CGAGGACCCGAAGATCGCTTAGGCAAGAATGGTGCTGATGAAATAAAAGCTCATCTTT TTCAACACCATCGACTTTTCCCGTGACATCCGAAAGCAGGCTGCACCCTACGTCCCCACC GAGGCCAGC - - - GGAGAGAGCGCCAAGGCCTGGGACACGCTGGCCTCCCCCAGCAGGCAAG 2958 2365 3018 3138 2358 1825 2478 1885 2538 1945 2598 2658 2778 2185 2838 2245 2898 2305 3078 2485 2545 2665 331'8 1765 2065 2718 2125 2425 2605 2725 3378 2782 δ

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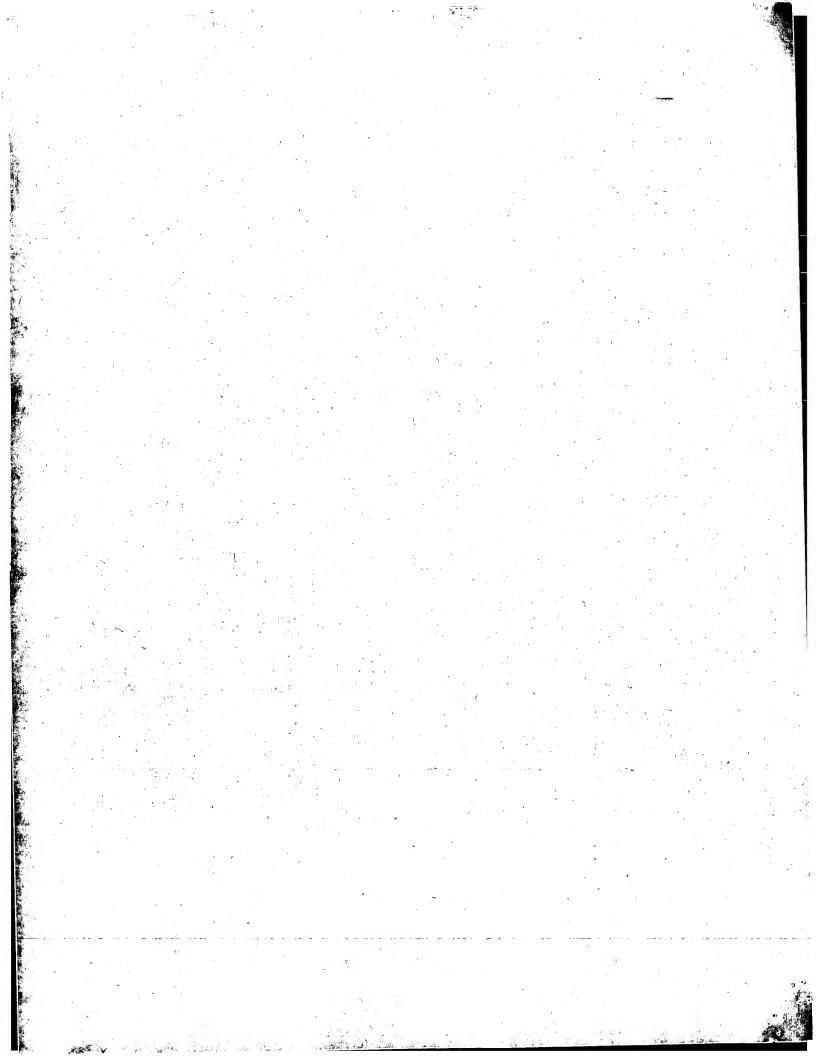
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CGCATCAAGAGTTACTCCCCTTATGCCTTCAAATTCTTCATGGAGCAACACGTGGAGAAT 1524
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                                                           the controlling Kindse Wart. IMPART, CHUR WAST. INCOLUGE.

human bone marrow CDMA library using PCR fragments of hWART1 as probes.

probes. 3 Polymorphisms were identified in the hWART1 gene: (1) at nuclectide 978, resulting in an Ala/Gly change; (2) at nuclectide 678, comprising a falletin of 2 adenosines, resulting in a C-terminal truncation of MART1 in the putative kinase domain. The latter frameshift hARRT1 in the putative kinase domain. The latter frameshift mutation was observed in 2 independent clones from human bone mutation was observed in 2 independent clones from human bone matation was observed in 2 independent clones from human cone. The control of hWART1 shows strong expression in cell lines from con small cell lung cancer, ovarian tumours, central nervous system one small cell lung cancer, ovarian tumours, and may provide a target tumors, renal tumours and breast tumours, and may provide a target tumors, renal tumours and breast tumours, and may provide a target tumors, renal tumours and breast tumours, and may provide a target tumors, renal tumours and breast tumours, and may provide a target con forcology drug development. Nucleic acids encoding full-length human to the man development and human development and human development. Segments 12-45, 55-151, 236-377, 404-520, 555-559, 601-702, 691-998 and 1011-1086, or lacking one or more of the N-terminal domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   hwarz sequences (AAX87397), hwarrl and hwarz polypeptides, a marthod for identifying modulators of hwarr function, and use of such modulator compounds to treat an abnormal condition involving hwarr signal transduction, especially cancer. Probes for detection of hwarr nucleic acids are also claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2117 TCAATCAGTAAGCTAGCAAAGAGGATCAGCCAAGCTTGCCCAAGGAAGATGAGAAGAA
of a cDNA clone coding for a human
                         (see AAY06526), of Drosophila non-receptor WART. hWART1 cDNA was isolated from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                      domain are claimed, as well as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 7382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7382 BP; 2291 A; 1458 C; 1417 G; 2216 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 760; DB 20;
Pred. No. 8.2e-187;
0; Mismatches 665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                catalytic domain, or C-terminal
                                    orthologue, i.e. hWART1 (see Pserine/threonine kinase WART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.18;
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Matches 1197; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          profit, immari; wawr orthologue; human; signal transduction; protein kinase; cancer; tumour; diagnosis; therapy; ss.
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/note= "results in Ala/Gly change"
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/note= "silent polymorphism"
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Db 24	Oy 164! Db 246:	Qy 17 Db 25			UY 18	Oy 18 Db. 27	Oy 19 0b 27	Qy 2005 Db 2822	Qy 2065 Db 2882	Oy 2125 Db 2942	Qy 2185 Db 3002	Oy 2245 Db 3062	Qy 2305 Db 3122	Oy 2365 Db 3182	Oy 2425 Db 3242	Oy 2485 Db 3302	Oy 2545 Db 3362	Oy 2605 Db 3422	Qy 26 Db 34

Search completed: January 16, 2003, 10:34:06 Job time: 464.423 secs



Title: Perfect score:

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APPLICANT: Zhang, Sheng
APPLICANT: Yu, Wan
TITLE OF INVENTION: NUCLEOTIDE AND PROFEIN SEQUENCES OF LATS
TITLE OF INVENTION: GENES AND METHODS BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036-Z711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/442,100
FILING DATE:
US-09-313-930-1

US-09-430-564-1

US-08-424-439-10

US-08-44-10487-10

US-08-464-954A-2

US-08-454-439-12

PCT-US94-1439-12

PCT-US94-1439-12

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US-09-289-466-1
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STREET: 1155 Avenue of the Americas
CITY: New York
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/411,111
                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-442-100-7; Sequence 7, Application US/09442100; Patent No. 6359193; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3155 base pairs
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REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET WUMBER: 65
TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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4: /cgn2_6/ptcdata/1/ina/6B_COMB.seg:*
5: /cgn2_6/ptcdata/1/ina/PCTUS_COMB.seg:*
6: /cgn2_6/ptcdata/1/ina/PCTUS_COMB.seg:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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                                                                                                                                                                                                                                                                                                          441362 seqs, 153338381 residues
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b; Pred. No. 0;
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Best Local Similarity 100.0%;
Matches 3155; Conservative 0 61 121 181 301 181 241 301 781 361 361 421 121 481 481 541 601 541 601 661 199 721 781 721 841 901 901 961 961 a 8 à ò ò 8 ò 셤 ô g ö a a D ô ò ъ. à <u>B</u>. ò g g ò ò a õ 8 ò 셤 ð g õ g ò g

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RESULT 2
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Pred. No. 0;
0; Mismatches
                                         APPLICANT: Virca, Duke
APPLICANT: Bird, Timothy A.
APPLICANT: Anderson, Dirk M.
APPLICANT: Marken, John S.
TITLE OF INVENTION: Human CDNAs Encoding Polse File Reference: 2877-US
CURRENT APPLICATION NUMBER: US/09/509,902A
CURRENT FILING DATE: 1999-08-03
NUMBER OF SEO ID NOS: 16
Sequence 15, Application US/09509902A Patent No. 6387676
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Pred. No. 8.6e-293;
0; Mismatches 196; Indels 9;
                                                                                                                         CURRENT APPLICATION NUMBER: US/09/509,902A CURRENT FILING DATE: 1999-08-03 NUMBER OF SEQ ID NOS: 16 SEQ ID NO 6 ELENGTH: 1498
                      Application US/09509902A 387676
                                                      APPLICANT: Virca, Duke
APPLICANT: Bird, Timothy A.
APPLICANT: Anderson, Dirk M.
APPLICANT: Marken, John S.
TITLE OF INVENTION: Human CDNAR
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86.38;
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Best Local Similarity 86.33
Matches 1295; Conservative
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; ORGANISM: HOMO Sapiens
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APPLICANT: Virca,
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                  718 AGACAGCCTGTACTTTGTGATGGACTACATCCCTGGTGGGGGGACATGATGAGCCTGCTGAT
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APPLICANT: Yau, Tian
APPLICANT: Tao, Wufan
APPLICANT: Anay, Weityi
APPLICANT: Zhang, Sheng
APPLICANT: Yu, Wan
TITLE OF INVEWTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS
TITLE OF INVEWTION: GENES AND METHODS BASED THEREON
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CORRESPONDENCE ADDRESS:
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New York
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STREET: 11
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10036-2711

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTCACCCTGTGAAGAGCGTGCGTGTGCTGCGGCCCGAGCCCCAGACAGCGGTGGGGGCCC 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1279 AAGAGTGCGGACAGT------GGTGACTCTGGGGATAAAGAAAGAAACAG 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGCATCAAGAGTTACTCCCCTTATGCCTTCAAATTCTTCATGGAGCAACACGTGGAGAAT 1524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1525 GTCATCAAAACCTACCAGCAGAAGGTCAGCCGGAGGCTACAGCTGGAGCAGGAAATGGCC 1584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1105 TCGCACCCCGCCTGGGTGGCTGCCCCACAGCACCTGCCACTGAGAGCCTGGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACCTGGACAGCCTGTGCACCAGTGTGCAGCAGAGTCTGCGAGGGGGGCACTGATCTAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1384 CGGATTCAGAGTTACTCCCCACAGGCCTTTAAGTTCTTCATGGAGCAGCACGTAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1039 ACCCATCCTTCTTGGATGCCACAGCCAGTTCAGACTGTTCAGCCTACCCCTTTTTCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGGGCAGCGCAGGCCCACACCCGCTGGATGTGGACTATGGCGGCTCCGAGCGCAGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1099 GGTACAGCTTCAAGTGTGCCTGTCATCCCACCTGTTGCTGAAGCTCCAAGCTATCAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1219 TCAGTAAGTAAGCCCTGCAAAGATGAACAGCCTAGCTTACCCAAGGAAGATGATAGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1345 GGGAGTGACAAGAGCCACAAAGGTGCGAAGGGGAGACAAAGCTGGCAGAGACAAAAAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTACAACTTCACCTATCACTGTTCGGAAAAACAAGAAGATGAAGAACGAAGAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCACCGCCTCCGTATCCAAAGCACTTGCTGCTGCCCAGTAAGTCTGAGCAGTACAGCGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 812.6; DB 4
Pred. No. 3.4e-204
REFERENCE/DOCKET NUMBER: 6523-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/411,111
                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                             NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
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65.1%;
                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 3213 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 1237; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
US-09-442-100-5
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 2524	OY 2665 ATCAGCCACCCATG	Qy 2725 GAGGCCAGCGGAGAG 	Qy 2782 CATCCAGAGCACGCC II I	OY 2842 CCCTTCCGGTGCCGG	RESULT 5 US-09-442-100-3 : Sequence 3. Application	INE TANT	APPLICANT: Wang, We APPLICANT: Zhang, Sl APPLICANT: Yu, Wan TITLE OF INVENTION:	TITLE OF INVENTION: NUMBER OF SEQUENCES: CORRESPONDENCE ADDRES; ADDRESSEE: Pennie	115 w Y ew US	ZIP: 10036-2711 COMPUTER-READABLE FOR MEDIUM TYPE: Flopp COMPUTER: IBM PC C	OPERATING SYSTEM: SOFTWARE: Patenting CURRENT APPLICATION IN APPLICATION IN APPLICATION NUMBER:	; FILING DATE: ; CLASSIFICATION: PRIOR APPLICATION DAT ; APPLICATION NUMBER:	FILING DATE: ATTORNEY/AGENT INFORM NAME: Misrock, S. REGISTRATION NUMBER	REFERENCE/DOCKET NU TELECOMMUNICATION INF TELEPHONE: (212) 7 TELEFAX: (212) 869	66 FO HA 3	TYPE: nucleic acid STRANDEDNESS: doub TOPOLOGY: unknown MOLECULE TYPE: cDNA	; FEATURE: ; NAME/KEY: CDS ; LOCATION: 231362 US-09-442-100-3	Query Match Best Local Similarity	
100			*						-				8	• • •		1			
9																	:		
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1503	1644	1704	1764	1824	1884	1944	2004	2064	2124	2184 <sup>°</sup> 2103	2244	2304	2364	2424	2484	2544 2463	2523	2664	
:	AAACTGGGCTCTGTGAGGCGGAGCAGGAGGAGAAGATGAGGAAGATCTCTACCAGAAGGGGGGT	TCTAACTACAACGGCTGAAGAGGCCAAGATGGACAAGTCCATGTTTGTGAAAATCAAG 	ACTCTAGGCATCGGTGCCTTTGGGGAAGTGTGCCTCGCTTGTAAGCTGGACACTCACGCT 	CTGTACGCCATGAAGACTCTCAGGAAGAAGATGTCCTGAACCGGAATCAAGTGGCCCAT 		TACTCCTTCCAGGACAGGACAGCCTGTACTTGTGATGGACTACATACCAGGGGGGAT 	ATGATGACCTGCTGATCAGGATGGAGGTCTTCCCTGAGCACCTGGCCGCTTCTACATT 	GCAGAGTTGACCCTGGCCATTGAAAGTGTCCACAAGATGGGCTTTATCCACCGGGACATC	AAGCCTGACAACATACTCATCGACCTGGATGGTCATATTAAGCTGACAGATTTTGGCCTC	TGCACTGGATTCAGGTGGACTCACAATTCCAAGTACTACCAGAAAGGGAACCACATGAGA 	CAGGACAGCATGGAGCCCGGTGACCTCTGGGACGATGTTTCCAACTGTCGCTGTGGAGAC :	AGGTTAAAGACCCTGGAGCAGAGGGCGCAGAAGCAGCACCAGAGGTGCCTGGCACTTCT ;	CTTGTCGGGACACCAAATTACATCGCTCCGGAGGTGCTTCTCCGCAAAGGGTACACGCAG .	CTCTGTGACTGGTGGAGCGTCGTGATTCTCTTTGAGATGCTGGTTGGGCAGCCGCCT .	CCCCACCCCAGAGAGGCAGAGAGGAGATCAACTGGGAGAGCACGCTG 	CATATCCCTACGCAGGTGAGGCTCAGCGCTGAGGCCCGAGACCTCATCACGAAGCTGTGC 2   1   1   1   1   1   1   1   1   1	TGCGCGGCTGACTGCCCCTGGGCAGGATGGGGCAGATGACCTCAAGGCACACCGGTTC 2   1   1   1   1   1   1   1   1   1	TTCAACACCATCGACTTTTCCGTGACATCCGAAAGCAGCTGCACCCTACGTCCCCACC	
1444 GTC	1585 AAAĢ	1645 TCT      1564 TCT	1705 ACTC     1624 ACA	1765 CTG       1684 TTG	1825 GTCP	1885 TACT      1804 TACT		-											
Db 14										2125	2185	2245	2305	2365	2425	2485	2545	2605	
Ω	o P	Oy Db	da G	Q D	oy D	Oy Op	g G	S P	oy D	S S	Sy B	Oy Dp	Qy Db	9 2	O. D.	S G	go Go	à	

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'AAGACCATCGATTTCTCTAGTGATCTGAGACAGCAGTCTGCTTCATACATCCCTAAA 2583
                              AGCCACCCCATGGACACCTCCAATTTTGACCCGGTGGATGAAGAAAGCCCCTGGCAC 2724
                                                                                        GCCAGCGGAGAG---AGCGCCAAGGCCTGGGACACGCTGGCCTCCCCCAGCAGCAAG 2781
                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENES AND METHODS BASED THEREON
                                                                                                                                                                                                                                     TTCCGGTGCCCGAAGCCCTCAGAGCCCGCAGAGT 2880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ER: IBM PC compatible
ING SYSTEM: PC-DOS/MS-DOS
RE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEE: Pennie & Edmonds
: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION DATA:
ATION NUMBER: 'US/09/442,100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6523-003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TICATION:
PLICATION DATA:
ATION NUMBER: 08/411,111
                                                                                                                                                                                                                                                                                                                     Application US/09442100 6359193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HONE: (212) 790-9090

AX: (212) 869-9741/8864

E 66141 PENNIE

ON FOR SEQ ID NO: 3:
E CHARACTERISTICS:
nucleic acid
DEDNESS: double
OGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y/AGENT INFORMATION:
Misrock, S. Leslie
TRATION NUMBER: 18,972
ENCE/DOCKET NUMBER: 652
MUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                             NT: Yu, Wan
F INVENTION: NUC;
F INVENTION: GENI
OF SEQUENCES: 16
ONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
231..3623
                                                                                                                                                                                                                                                                                                                                                                      : Xu, Tian
: Tao, Wufan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y: USA
10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New York
                                                                                                                                                                                                                                                                                                                                                        FORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE:
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24.1%; Score 760; DB 4; Length 3984; 53.7%; Pred. No. 2.6e-190;

Oy 2065 AAGCC 	2125	Db 2778 TGCAC		Oy 2245 AGGTT2         Db 2898 AGACTC	0y 2305 crrdro         Db 2958 rrdgr			3138	0y 2545 rgcgcc         Db 3198 CGAGG	3258	Oy 2665 ATCAGG        Db 3318 ATCAC?	3378	Qy 2782 CATCCA               Db 3438 CATCCI	Oy 2842 CCCTTC         Db 3498 CCATAI	RESULT 6 US-09-442-100-1 ; Sequence 1, Ap	; Patent No. 635; GENERAL INFOR APPLICANT: APPLICANT:		TITLE OF IN NUMBER OF S CORRESPONDE ADDRESSEE	
•				,			-		•				-					<del></del>	
	CACTCTGCTAATTCTCAGCCTTCTGCTACAACA CTTCACCTGTGAAGAGCGTGCGTGTGCTGCGG		5 TCGCACCCCGCCTGGGTGGGTGCGCCCACAGCACCTGCAGAGGCCTGGAGAGCGAGG 1164 	6 GAGGGCAGCGCCACCACCCGCTGGATGTGGACTATGGCGGCTCCGAGCGCAGGTGC 1224	CCACCGCCTCGTATCCAAAGCACTTGCTGCTGCTGCTAAGTCTGAGCAGTACAGCGTG	GACCTGACAGCCTGTGCACCAGTGTGCAGCAGAGGTCTGCGAGGGGGCACTGATCTAGAC	GGGAGTGACAAGACCACAAAGGTGCGAAGGGAGACAAAGCTGGCAGAGACAAAAGCAG 1404 	ATTCAGACCTCCCGGTGCCTGTCCGCAAGAATAGCAGAGATGAAGAAAGA	CGCATCAAGAGTTACTCCCCTTATGCCTTCAAATTCTTCATGGAGCAACACGTGGAGAAT 1524	GTCATCAAAACCTACCAGCAGAAGGTCAGCGGAGGCTACAGCTGGAGCAGGAAATGGCC 1584	AAAGCTGGGCTCTGTGAGGCCGAGCAGAGCAGATGAGGAAGATCCTCTACCAGAAGGG 1644 	TCTAACTACCGGCTGAAGAGGGCCAAGATGGACAAGTCCATGTTTGTGAAAATCAAG 1704 	ACTCTAGGCATCGGTGCCTTTGGGGAAGTGTGCCTCGCTTGTAAGCTGGACACTCACGCT 1764	CTGTACGCCATGAAGACTCTCAGGAAGATGTCCTGAACGGAATCAAGTGGCCCAT 1824	GTCAAGGCTGAGAGGACATCCTGGCTGAAGCAGACAATGAGTGGGTGG	TACTCCTTCCAGGACAAGGACAGCCTGTACTTTGTGATGGACTACATACCAGGCGGGGAT 1944 	ATGATGAGCCTGCTGATCAGGATGAGGTCTTCCCTGAGCACCTGGCCCGCTTCTACATT 2004	GCAGAGTTGACCCTGGCCATTGAAAGTGTCCACAAGATGGCTTTATCCACCGGGACATC 2064 	
Mat	Db 1653 Qy 1045	Db 1713	Oy 1105 Db 1773	Oy 1165 Db 1833	Oy 1225 Db 1893	Oy 1285 Db 1953	Qy 1345 Db 2013	Oy 1405 Db 2058	Qy 1465 Db 2118	Qy 1525 Db. 2178	Qy 1585 Db 2238	Qy 1645 Db 2298	Qy 1705 Db 2358	Oy 1765 Db 2418	Oy 1825 Db 2478	Qy 1885 Db 2538	Oy 1945 Db 2598	Qy 2005 Db 2658	

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ACAGCATGGAGCCCGGTGACCTCTGGGACGATGTTTCCAACTGTCGCTGTGGAGAC 2244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGGCCCCCCACACACAGAGGCGCAGCTGAAGGTGATCAACTGGGAGAGCACGCTG 2484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGCTGACTGCCGCCTGGCCAGGGATGGGGCAGATGACCTCAAGGCACACCCGTTC 2604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAGCACGCCTTCTATGAGTTCACCTTCCGCAGGTTCTTCGATGACAACGGCTAT 2841
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                                                                                                                                                                                  CTGGATTCAGGTGGACTCACAATTCCAAGTACTACCAGAAAGGGAACCACATGAGA 2184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IAAAGACCCTGGAGCAGAGGGCGCAGAAGCAGCACCAGAGGTGCCTGGCACATTCT 2304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIGACTGGTGGAGCGTCGGTGTTTCTCTTTGAGATGCTGGTTGGGCAGCCGCCT 2424
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NNT: Tao, Wufan

NNT: Wang, Weiyi

NNT: Wang, Weiyi

NNT: Yu, Wan

NUT: Yu, Wan

NUT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09442100
359193
ORMATION:
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ATAATTATCCGAAGCC 3517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGGTGCCCGAAGCC 2861
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TGTCCTGAACCGGAATCAAGTGGCCCATGTCAAGGCTGAGAGGGACATCCTGGCTGAAGC 1856

1797

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1796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -AGAGATGAAGAGAAGAGAGTCTCGCATCAAGAGTTACTCCCCTTATGCCTTCAAATT 1499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTCATGGAGGAACACGTGGAGAATGTCATCAAAACCTACCAGCAGAAGGTCAGCGGAG 1559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2869 GGGCGCGAATAGCTCGGGCGGCAGCAACGGATCCACCGCCACCACCGCCTCCTCGTCGAC 2928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1329 GGGCACTGATCTAGACGGGAGTGACAAGAGCCACAAAGGTGCGAAGGGAGACAAAGCTGG 1388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1740 CGCTTGTAAGCTGGA---CACTCACGCTCTGTACGCCATGAAGACTCTCAGGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTACAGCTGGAGCAGGAAATGGCCAAAGCTGGGCTCTGTGAGGCCGGAGCAGGAGCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2989 GAAGGAGGAGGAGCGCAAGGAGTTCCGCATCAGGCAGTACTCGCCGCAAGCCTTCAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 5720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                       Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 564.6; DB 4;
Pred. No. 9.1e-139;
Mismatches 494;
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                            NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6523-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9990
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                    APPLICATION NUMBER: US/09/442,100
                                                                                                                       PC-DOS/MS-DOS
                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/411,111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.98;
64.48;
                                                                                                                                                                                                                                                                                                                                                               TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               5720 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 64.4
Matches 979; Conservative
                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
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1103..4402
                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
                                                                                                                         OPERATING SYSTEM:
                                   New York
                                                              10036-2711
                   New York
                                                   USA
                                                                                                                                                                                                                                                  FILING; DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY:
; LOCATION:
US-09-442-100-1
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                                                                                                                                                                                                                                  2334 GGAGGTGCTTCTCCCCAAAGGGTACACCCAGCTCTGTGACTGGTGGAGCGTCGGTGAT
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                                                                                TGTGATGGACTACCATACCAGGCGGGATATGATGAGCCTGCTGATCAGGATGGAGGTCTT
                                                                                                                                CCCTGAGCACCTGGCCCGCTTCTACATTGCAGAGTTGACCCTGGCCATTGAAAGTGTCCA
AGACAATGAGTGGGTGGTCAAACTCTACTACTCCTTCCAGGACAAGGACAGCCTGTACTT
                                         CCGCAGGTTCTTCGATGACAA 2834
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CCGTCGCTTCTTCGACGACAA 4356

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TTGGCCTCTGCACTGGATTCAGGTGGACTCACAATTCCAAGTACTACCAGAAAGGGAACC 2176
TITLE OF INVENTION: Fungal Target Genes and Methods FILE REFERENCE: PB/5-30908A
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Pred. No. 2e-58;
0; Mismatches 447;
                                               2158
                                             CURRENT APPLICATION NUMBER: US/09/588,256
CURRENT FILING DATE: 2000-06-06
                                                                                                                                                       Sequence 1, Application US/09588256 Patent No. 6291665
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                                                                                                                                                                                                                                                                    Yasmina
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Wendland, Juergen
Ayad-Durieux, Yası
                                                                                                                                                                                                                                                                                                 Philippsen, Peter
                                                                                                                                                                                                      Gaffney, Thomas
Flavier, Albert
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Best Local Similarity 54.64
Matches 598; Conservative
                                                                                                                                                                                                                                                                                   Dietrich, Fred
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Ashbya gossypii
                                                                                                                                                                                                                                                                                                                                                                                              Patentin Ver.
                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (1)..(2160)
US-09-588-256-1
                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                        US-09-588-256-1
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APPLICANT:
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                                                                                                                                                                                                                           APPLICANT: Mondahar, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT APPLICATION NUMBER: US 60/088,801
EARLIER PILING DATE: 1999-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
LENGTH: 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 333; DB 4; Length 63
Pred: No. 3.4e-78;
0; Mismatches 180; Indels
                           Sequence 26, Application US/09328111 Patent No. 6262333
                                                                                                                      Burgess, Christopher C. Bushnell, Steven E.
                                                                       Endege, Wilson O.
Steinmann, Kathleen
Astle, Jon H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.6%;
71.3%;
                                                                                                                                     Bushnell, Steven E.
Carroll III, Eddie
Catino, Theodore J.
                                                                                                                                                                                                                   Lewis, Marcia E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 71.3
Matches 454; Conservative
                                                                                                                                                                                   Derti, Adnan
Ford, Donna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
US-09-328-111-26
         .09-328-111-26/c
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38
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2549 CGGCJGACTGCCCCCTGGGCAGGGATGGGGCAGATGACCTCAAGGCACACCCGTTCTJCA, 2608
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1355 TCGGTCTGTCGACAGGGTTCCACAAACGCATGACTCCAACTACTACAAGAAGCTGCTTC 1414
                                                                                                                           1475 GCGGCAACGGCGGCGAACAGAAAAACACCATGCTTGTCGACGCCATCCACCTGACCATGA 1534
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                                                            1415 AGGAGGACGAGCAGCAGCAGAACGGCGGAACATGGGCAAATATCCCGCATCCGGTGGCG
                                ACATGAGACAGGACAGGAGCCCGGTGACCTCTGGGACGATGTTTCCAACTGTCGCT
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3174 Porter Drive
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Patent No. 5885803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bandman, Olga
Hillman, Jennifer L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: DISEASE TITLE OF INVENTION: KINASES
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Shah, Purvi
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APPLICATION NUMBER: US,
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2669 GCCACCCATGGACAC 2684
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ADDRESSEE: Incyte P
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APPLICANT: Bandma
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CITY: P
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                                                                                                                                                                                                                                                                                                                                                                   Length 1935;
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                                                                                                                                                                                                                                                                                                                                                                   Score 233.8; DB 2;
Pred. No. 7.4e-52;
0; Mismatches 532;
                                                                                            REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                      J.4%;
Best Local Similarity 51.7%;
Matches 609; Conservative (
                                                               ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1935 base pairs
                                                                                                                                                           TELEFAX: 415-845-4166
                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
PRIOR APPLICATION: 435
APPLICATION DATA:
APPLICATION NUMBER:
FILING DAMP
                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: sing
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LIBRARY: SYNORATO4
CLONE: 705365
                                                                                                                                                                                                                                                                               linear
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AGTGAÇTTCTCATTTC TGGAGCAGAGGCGCA	TTACAT	CGTCGC 	CACAGA      TCAAGA	GAGGCT	CCTGGG	TTCCCG																					
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TGAATTTTATAGAAATCTCACACACACCCACCAAGTGACTTCTCATTTC GGACGATGTTTCCAACTGTCGCTGTGGAGACAGGTTAAAGACCCTGGAGCAGAGGGCGCA	AACATGAACTCAAGGGAAAGCAGAAACTTG	GGAGGTGCTTCCGCAAAGGTACACGCAGCTCTGTGACTGGTGGAGCGTCGGTGTGAT 	TCTCTTTGAAATGCTGGTTGGCAGCCGCCTTTCTTGGCCCCCACCCCACCAGAGAGACAA 	GCTGAAGGTGATCAACTGGGAGGAGCACGCTGCATATCCCTACGCAGGTGAGGCTCAGCGC	TGAGGCCCGAGACCTCATCACGAAGCTGTGCTGCGCGGCTGACTGCCGCCTGGCAGGA	TGGGGCAGATGACCTCAAGGCACCCGTTCTTCAACACCCATGGACTTTTCCCGTGACAT	3C 2670	il 30 1261						•	ASSOCIATED PROTEIN		.;					2.0		,			
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TGAATTTTATAGAAATCTCACACACAAGCCCACCA GGACGATGTTTCCAACTGTCGCTGTGGAGACAGG	HI HIH HIH HIH HABAGABABGABABCTTG GAACAGCACACAGGGGGGCGGGAATTCTCTT( HIH HIH HIH HIH HIH HIH GAAGAAGAGACACA	ACACGC       	AGCCGC        ATCCAC	GCACGC      AAACTC	AGCTGT     GATTTT	ACCCGT	TCCCCA	I TAGAAA		72796	٠				ASSOC		Incyte Pharmaceutical					dows Ve	us/09/272,796		9,989		49 PF-0321
TCACAC	AGGAAA GCCTGG           AACTGG	AAGGGT	TTGGGC       TAGGAT	GGGAGA       GGAAAG	rcacga      TCTCA	AGGCAC	CTACG	- rcccta:	•	.ze/035	Olga	Jennifer Jeil C.	r.	κ.	DISEASE	21,	harmace Drive			. a	bos DOS	FastSEQ for Windows CATION DATA:	60/sn		08/878,989	FION:	36,74
GAAATC	TCAAAG AGAGGT      GGAGAC	TCCGCA 	TGCTGG      TGCTAA	GTGATCAACTGG 	AGACCTCA            GGACTTAA	ACCTCA 	CTGCAC	CAGCAA		ation	N	- 2	Guegler, Karl Lal, Preeti	, Surya	i	CES:	: Incyte Pharmac 3174 Porter Drive	£ £		E FORM:	É.	ESEQ for	MBER:	: A DATA	(BER:	NFORMA'S, Lucy	JMBER: ET NUM
TTTATA	ATGAÁC AGCACC II II AGAACA	TGCTTC     TATTCA	TTGAGA          ATGAAA	AGGTGA               AAGTGA	cccaag     ccaagg	CAGATG	AGCAGG	GGCCAGC	· .	Applica 07148	RMATION: Bandman.	Hillman, Corley,	Gueg	Goli,	TITLE OF INVENTION:	NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS	E: Inc	Palo Alto	Y: USA	ABI		SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:	APPLICATION NUMBER:	CLASSIFICATION: PRIOR APPLICATION DATA:	TON NU	ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J J	REGISTRATION NUMBER: 36 REFERENCE/DOCKET NUMBER:
									-796-1	e 11, N	NERAL INFO	APPLICANT:	APPLICANT:	APPLICANT:	E OF I	NUMBER OF	ADDRESSEE:	61	TR	MPUTER RI	COMPUTER:	SOFTWARE	APPLICATION FILING DATE	ASSIFIC R APPI	PLICAT LING D	RNEY/A	SISTRA
781	831 2274 865	2334	2394	2454	2514	2574	2634	1225	RESULT 10	Sequence 11, Application US/09272796	GENERAL INFORMATION: APPLICANT: Bandma	APPL	APPL	APPL	TITLE	NUMB	AD	CITY	COUN	COMP	0 6	SOCURR	AP	CL	AP	ATTO	RE
oy Oy	do oy	Oy Db	Qy Db	Oy Db	Oy Db	Qy	δŏ	qq	RES	S		· · · ·															. •• ••

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                                                                                                                                                                                                                                                                                             Length 1935;
                                                                                                                                                                                                                                                                                                                                      Indels.
                                                                                                                                                                                                                                                                                           7.4%; Score 233.8; DB 4; 51.7%; Pred. No. 7.4e-52; ative 0; Mismatches 532;
### 415-855-0555

ATT | 415-845-4166
                                                                              IN FOR SEQ ID NO: 11:
                                                                                              E CHARACTERISTICS:
TH: 1935 base pairs
nucleic acid
DEDNESS: single
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TE SOURCE:
RY: SYNORAT04
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ACCGGAATCAAGTGGCCCATGTCAAGGCTGAGAGGGACATCCTGGCTGAAGCAGACAATG 1864
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 GAAGAAGAACAGGAGACAACTGGCATATTCCACAGTTGGGACACCAGATTACATTGCTCC 924
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                                                                                                        TCTCTTTGAGATGCTGGTTGGCCAGCCGCCTTTCTTGGCCCCCACCCCCACAGAGACGCA
                                  2334 GGAGGTGCTTCTCCGCAAAGGGTACACGCAGCTCTGTGACTGGTGGAGGGTCGGTGAT
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                                                                   AGAAGTATTCATGCAGACTGGTTACAACAAATTGTGTGACTGGTGGTCTTTGGGAGTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hemmings, Brian A.
APPLICANT: Millward, Thomas A.
TITLE OF INVENTION: Nuclear DBF2-Related (NDR) Kinases
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Pred. No: 1.7
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CURRENT APPLICATION NUMBER: US/08/860,150B
CURRENT FILING DATE: 1997-06-19
EARLIER APPLICATION NUMBER: PCT/EP95/05052
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EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: 94810746.1
EARLIER FILING DATE: 1994-12-22
NUMBER OF SEQ ID NOS: 18
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Best Local Similarity 52.2%;
Matches 577; Conservative
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TOTATION: (596)..(1990)
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US-08-860-150-6
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TITLE OF INVENTION: Nuclear DBF2-Related (NDR) Kinases
FILE REFERENCE: 4-20265/A/PCT
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Patent No. 6040164
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APPLICANT: Hemmings, Brian A.
APPLICANT: Millward, Thomas A.
TITLE OF INVENTION: Nuclear DBF2-Related (NDR) Kinases
FILE REFERENCE: 4-20265/A/PCT
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CURRENT FILING DATE: 1997-06-19
EARLIER APPLICATION NUMBER: PCT/EP95/05052
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: 94810746.1
EARLIER FILING DATE: 1994-12-22
NUMBER OF SEQ ID NOS: 18
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Matches 557; Conservative
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US-08-860-150-1
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LENGTH: 2101
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US-08-860-150-1
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                                                                                                                                                                                                                                                                                                                  Score 225.2;
Pred. No. 1.7
EARLIER FILING DATE: 1997-06-19
EARLIER APPLICATION NUMBER: PCT/EP95/05052
EARLIER FILING DATE: 1995-12-20
EARLIER FILING DATE: 1994-12-22
NUMBER OF SEQ ID NOS: 18
SOFWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                  7.1%;
darity 52.2%;
Conservative
                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: (596)..(1990)
US-09-338-132-6
                                                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Simidarity
Matches 577; Conserv
                                                                                                                                                            LENGTH: 3018
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1860 CAATGAGTGGTCGAAACTCTACTACTTCCAGGACAAGGACAGCCTGTACTTTGT 1919
                                               GATGGACTACATACCAGGCGGGGATATGATGAGCCTGCTGATCAGGATGGAGGTCTTCCC 1979
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                   AGATGACCTCAAGGCACACCCGTTCTTCAACACCATCGACT 2620
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GENERAL INFORMATION.

APPLICANT: Hamings, Thomas A.

APPLICANT: Hamings, Thomas A.

TILE OF INVENTION NUCLEAR DBF2-Related (NDR) Kinases

FILE REFERENCE: 4-20265/A/PCT

CURRENT APPLICATION NUMBER: US/09/338,132

CURRENT APPLICATION NUMBER: US/09/338,132

CURRENT APPLICATION NUMBER: 08/860,150

EARLIER FILING DATE: 1997-06-19

EARLIER FILING DATE: 1997-06-19

EARLIER APPLICATION NUMBER: PCT/EP95/05052

EARLIER APPLICATION NUMBER: 94810746.1

EARLIER FILING DATE: 1994-12-22
                                     Sequence 1, Application US/09338132 Patent No. 6040164
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                                                                                                      GENERAL INFORMATION:
RESULT 14 'US-09-338-132-1
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                                                                                                    30;
                                                                           Length 2101;
                                                                                                      Indels
                                                                                                       .0; Mismatches 474;
                                                                                 DB 3;
                                                                                Score 222.6; DB 3
Pred: No. 6.9e-49;
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TYPE: DNA
ORGANISM: Drosophila melanogaster
FEATURE:
                                                                                 Query Match 7.1%;
Best Local Similarity 52.5%;
Matches 557; Conservative
                                   ; NAME/KEY: CDS
; LOCATION: (132)...(1499)
US-09-338-132-1
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2460 GGTGATCAACTGGGAGACGCTGCATATCCCTACGCAGGTGAGGCTCAGGGCTGAGGC 2519
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Pred. No. 6e-47;
0; Mismatches 138; Indels 2
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                                                                                                                                                       2580 AGATGACCTCAAGGCACACCCGTTCTTCAACACCATCGACT 2620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
                                                                                                                                                                                                                                                                                              Sequence 66, Application US/09328111 Patent No. 6262333
                                                                                                                                                                                                                                                                                                                                                                                                             Burgess, Christopher C.
Bushnell, Steven E.
Carroll III, Eddie
Catino, Theodore J.
Derti, Adnan
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OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                     Endege, Wilson O.
Steinmann, Kathleen E.
Astle, Jon H.
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Best Local Similarity 68.8%;
Matches 308; Conservative
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FITLE OF INVENTION: PRODUCTS
FILE REFERENCE! CCD-257 (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lewis, Marcia E.
Monahan, John E.
Schlegel, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ord, Donna M.
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OM nucleic - nucleic search, using sw model

Run on:
January 16, 2003, 09:56:42; Search time 87:5516 Seconds

(without alignments)
16067.254 Million cell updates/sec

Title:
WS-09-763-334-5
Ferfect score:
3155
Sequence:
1 algagagccaccccgaagtt.....aagagcacttatttggggg 3155
Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0
Searched:
393868 seqs, 222934149 residues
Total number of hits satisfying chosen parameters:
787736
Minimum DB seq length: 0
Maximum Match 0%-
Maximum Match 100%
Dost-processing: Minimum Match 100%
Listing first 45:summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq. /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq. /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq. /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.

ptodata/2/pubpna/US07\_NEW\_PUB.seq: ptodata/2/pubpna/PCTUS\_PUBCOMB.seq: ptodata/2/pubpna/US08\_NEW\_PUB.seq: ptodata/2/pubpna/US08\_NEW\_PUB.seq: ptodata/2/pubpna/US09\_NEW\_PUB.seq: /ptodata/2/pubpna/US09\_PUBCOMB.seq:

/pubpna/PCT\_NEW\_PUB.seq:/ /pubpna/US06\_NEW\_PUB.seq

Published\_Applications\_NA:

Database :

/cgn2\_6/p

## SUMMARIES

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Res	Result	*	Query				
	No.	Score	Match	Match Length DB	DB	ID	Description
	1	1035.2	32.8	2043	6	US-09-836-392-2	Sequence 2, Appli
	N	546.6	17.3	929	6	US-09-764-868-214	Sequence 214, App
Ü	m	333	10.6	638	10	US-09-879-536-26	Sequence 26, Appl
	4	231.2	7,.3	1689	6	US-09-938-842A-1861	_
	Ŋ	228	7.2	1452	6	US-09-938-842A-2402	Sequence 2402, Ap
	9	225.2	7.1	3583	6	US-09-974-298-152	Sequence 152, App
	7	214.4	9.9	678	10	US-09-879-536-66	Sequence 66, Appl
	œ	192.2	6.1	734	6	US-09-764-868-196	
	σ	169.4	5.4	1818	10	US-09-771-161A-89	
	10	161.8	5.1	2549	. 10	US-09-880-107-3691	Н
	11	155.6	6.4	1635	10	US-09-880-107-2340	Sequence 2340, Ap
	12	149.8	4.7	3407	10	US-09-971-845-1	Sequence 1, Appli
	13	142	4:5	1398	6	US-09-938-842A-633	3
	14	138.8	4.4	1416	6	US-09-938-842A-2503	Sequence 2503, Ap
	15	135.6	4.3	1735	6	US-09-764-868-58	Sequence 58, Appl
	16	134.8	4.3	1.244	10	US-09-771-161A-38	
	17	134.8	4.3	1393	10	US-09-771-161A-37	7
	18	133.6	4.2	1257	10	US-09-799-875-15	Sequence 15, Appl
	19	133.6	4.2	1826	10	US-09-799-875-13	Sequence 13, Appl

Sequence 166, App	Sequence 2146, Ap	Sequence 3, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 1, Appli	3, 8	Sequence 1, Appli	Sequence 8122, Ap	Sequence 293, App	Sequence 2043, Ap	Sequence 571, App	Sequence 571, App		Sequence 3, Appli	Sequence 7789, Ap	Sequence 527, App	Sequence 1, Appli	Sequence 46, Appl	Sequence 6230, Ap	Sequence 297, App	Sequence 4, Appli	Sequence 6, Appli	Sequence 10, Appl	Sequence 8, Appli	Sequence 1, Appli
9 US-10-098-841-166	10 US-09-880-107-2146	10 US-09-970-000-3	10 US-09-804-471A-1	1:2 US-10-028-946-3	12 US-10-028-946-1	9 US-10-017-216-3	9 US-10-017-216-1	9 US-09-796-692-8122	10 US-09-864-864-293	10 US-09-294-093B-2043	9 US-10-174-590-571	9 US-10-176-758-571	12 US-10-052-586-571	9 US-09-836-392-3	9 US-09-796-692-7789	10 US-09-954-456-527	10 US-09-842-307-1	10 US-09-771-161A-46	10 US-09-867-701-6230	10 US-09-801-368-297	10 US-09-841-683-4	10 US-09-841-683-6	10 US-09-841-683-10	10 US-09-841-683-8	10 US-09-801-876B-1
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4.2	4.1	4.0	4.0	4.0	4.0	. 3.9	3.9	3.8	3.8	3.8	3.8	3.8	3.8	3.7	3.7	3.5	3.5	3.4	3.4	3.4	3,3	3.3	3.3	3.3	3.3
133.6	129.2	126.4	125.8	125.8	125.8	122.6	122.6	120.2	120.2	119.8	118.4	118.4	118.4	118.2	118	111.8	111.8	108:4	106.6	105.8	103.4	103.4	103.4	103.4	103.4
20	21	22	23	24	25	- 56	27	28	29	. 30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT	
-60-Sn	US-09-836-392-2
Sear	uence 2, Application US/09836392
· ; Pate	Patent No. US20020173458A1
GENE	GENERAL INFORMATION:
; API	APPLICANT: Ruben et al.
; TIT	TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypeptides
LIT ;	FLE OF INVENTION: Antibodies
; FII	FILE REFERENCE: PT020P1
COL	CURRENT APPLICATION NUMBER: US/09/836,392
; cur	CURRENT FILING DATE: 2001-04-18
; PRI	PRIOR APPLICATION NUMBER: PCT/US00/28066
; PR1	
; PR1	
; PR	
; PR1	APPLICATION N
; PR1	PRIOR FILING DATE: 1999-11-17
; PR	PRIOR APPLICATION NUMBER: 60/189,027
; PR1	PRIOR FILING DATE: 2000-03-14
NON :	NUMBER OF SEQ ID NOS: 34
; SOF	SOFTWARE: Patentin Ver. 2.0
; SEQ	SEQ ID NO 2
; :	LENGTH: 2043
T. T.	TYPE: DNA
, o	ORGANISM: Homo sapiens
-60-SD	US-09-836-392-2
Onez	Ouery Match 32.8%; Score 1035.2; DB 9; Length 2043;
Best	18; Pred. No. 8.2e-271;
Matc	Matches 11/0; Conservative 0; Mismatches 188; Indels 12; Gaps 1;
Qy 1	1585 AAAGCTGGGCTCTGTGAGGCCGAGCAGGAGCAGATGAGGAAGATCCTCTACCAGAAGGAG 1644
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3	AATGCTGGACTCTGTGAAGCTGAGGAGCAGATGCGGAAGATCCTCTACCAGAAAGA
0у 1	1645 TCTAACTACAACCGGCTGAAGAGGGCCCAAGATGGACAAGTCCATGTTTGTGAAAATCAAG 1704
QQ	275 TCTAATTACAACAGGTTAAAGAGGGCCAAGATGGAGAGGTCTATGTGTGAGATCAAA 334
0y 1	1705 ACTCTAGGCATCGGTGCCTTTGGGGAAGTGTGCCTCGCTTGTAAGCTGGACACTCACGCT 1764
QQ	335 ACCTGGGGGGCTTTTTTTTTTTTTTTTTTTTTTTTTTTT
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Pred. No. 1.8e-138;
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                                                                                                                                                                                                   Proteins,
                                                                                                                                                                                    APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteir
FILE REFERENCE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILLING DATE: 2001-01-17
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  2845 TTCCGGTGCCCGAAGCCCTCAG-
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SEQ ID NO 214
LENGTH: 676
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Best Local Similarity 89.5
Matches 607; Conservative
                                                                                                                                                Sequence 214, Application Patent No. US20020168711A1
                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (628)
; OTHER INFORMATION:
US-09-764-868-214 ;
                                                                                                                                                                         GENERAL INFORMATION:
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US-09-764-868-214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1525 GTCATCAAAACCTACCAGCAGAAGGTCAGCCGGAGGCTACAGCTGGAGCAGGAAATGGCC 1584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTCTAGGCATCGGTGCCTTTGGGGAAGTGTGCCTTCGCTTGTAAGCTGGACACTCACGCCT 1764
                                                                    CTGTACGCCATGAAGACTCTCAGGAAGAAGGATGTCCTGAACCGGAATCAAGTGGCCCCAT 1824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1885 TACTCCTTCCAGGACAAGGACAGCCTGTACTTTGTGATGGACTACATACCAGGCGGGGAT 1944
TCTAATTACATCCGTCTTAAAAGGGCTAAAATGGACAAGTCTATGTTTGTGTGAAGATAAAG 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          637 GTACTCAAATCTCATCAGCAGCGTCTACATCGTAAAAAACAATTAGAGAATGAAATGATG 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             577 CGGGTTGGATTATCTCAAGATGCCCAGGATCAAATGAGAAAGATGCTTTGCCAAAAAGAA 518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGTATGCAACAAAACTCTTCGAAATAAAGATGTTCTTCTTCGAAATCAAGTCGCTCAT 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 333; DB 10;
Pred. No. 1.6e-80;
0; Mismatches 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lewis, Marcia E.
APPLICANT: Mondhan, John E.
APPLICANT: Schlegel, Robert
TILE OF INVENTION: NOVEL HUMAN GENES AND GENE
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/879,536
CURRENT FILING DATE: 2001-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NG DATE: 2001-09-21
ATION NUMBER: US 60/088,801
DATE: 1998-06-10
                                                                                                                                                                                                                                       Sequence 26, Application US/09879536
Patent No. US20020144298A1
                                                                                                                                                                                                                                                                                                                                            Burgess, Christopher
Bushnell, Steven E.
Carroll III, Eddie
Catino, Theodore J.
                                                                                                                                                                                                                                                                                        Endege, Wilson O.
Steinmann, Kathleen
Astje, Jon H.
                                                                                                                    2152 TCCAAGTACTACCAGAAA 2169
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ilarity 71.3%;
Conservative
                                                                                                                                        659 TTCCAATATTACCAGAAA 676
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                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Fast
SEQ ID NO.26
LENGTH: 638
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Best Local 3
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APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS_CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
FULE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1504 ATGGAGCAACACGTGGAGAATGTCATCAAAACCTACCAGCAGAAGGTCAGCCGGAGGCTA 1563
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                                                                                                                                                                                                                                                                                                   2121
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                                                                               1945 ATGATGAGCCTGCTGATCAGGATGGAGGTCTTCCCTGAGCACCTGGCCCGCTTCTACATT 2004
                                                                                                                                                                                       2005 GCAGAGTIGACCCTGGCCATIGAAAGIG---ICCACAAGAIGGGCITTAICCACCGGGAC 2061
217 ATGATGAGCCTATTAATTAGAATGGGCATCTTTCCAGAAAGTCTGGCACGATTCTACATA 158
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                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                           2122 CTCTGCACTGGATTCAGGTGGACTCACAATTCCAAGT 2158
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                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR PELICATION NUMBER: US 60/264,647
PRIOR PELICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1861, Application US/09938842A Patent No. US20020160378A1
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US-09-938-842A-1861
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51.8%;
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Matches 580; Conservative
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APPLICANT: Harper, Jeff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Joel
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JS-09-938-842A-1861
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ORGANISM:
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1433 AGAATAGCAGAGATGAAGAGAAGAGAGTCTCGCATCAAGAGTTACTCCCCTTATGCCT 1492
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                                                                                                                                                                                                                                                                               143 AGAGACGGTGGATCTTAGAAAGAAAGTTGGCGTCTTCTGGAGTGCCAAAAGAGGGAGCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 AGATTAGTGTCGATGACTTTGAGCTTTTGACTATCGTAGAGAGGTGCTTTTGGTGAGG
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                                                                                                                                                                                                                          Mismatches 640;
                                                                                                                                                                                          Score 228; DB 9;
Pred. No. 8.4e-52;
                                60/300,111
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                                                                                                                              ORGANISM: Arabidopsis thaliana
                          NUMBER: US 6
2001-06-22
                                                                                                                                                                                        7.28;
                  PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2001-06-2
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2402
LENGTH: 1452
                                                                                                                                                                                                   Best Local Similarity 49.7
Matches 638; Conservative
                                                                                                                                                US-09-938-842A-2402
                                                                                                               TYPE: DNA
                                                                                                                                                                                    Query Match
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APPLICANT: Kreps, Joe1
APPLICANT: Kreps, Joe1
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING:
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF ILING DATE: 2001-08-24
CURRENT FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING: DATE: 2000-08-24
PRIOR FILING: DATE: 2001-01-16
                                                                                                                        1983
                                                                                                                                                                             1984 CACCTGGCCCGCTTCTACATTGCAGGTTGACCCTGGCCATTGAAAGTGTCCACAAGATG 2043
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                                                                                                                                                                                                                                                                         12 AATTAGGTCCACAGGGATATAAAGCCTGATAATTATTGATTACTCGAAACGGCATATC 771
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472 CGACGAGGGCAGGTGGAACATGTTAAAGCTGAAAGAAATGTGCTTGCAGAAGTGGATAGC
                                   1864 GACTGGGTGGTCAAACTCTACTACTCCTTCCAGGACAAGGACAGCCTGTACTTTGTGATG
                                                                                                         GACTACATACCAGGGGGGTATGATGAGCCTGCTGATCAGGATGGAGGTCTTCCCTGAG
                                                                                                                                CCTITCAITGICAAGCITIGITACICITICCAAGAIGAGAGCAITIGIATTATTAIG
                                                                                                                                                                                                     652 GATGAGACTCGGTTTTATGTTGCGGAGACAATTCTGGCTATTGAGTCTATCCATAAGCAT
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Patent No. US20020160378A1
GENERAL INFORMATION:
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    AAAAAGAGCAGGTTGGCCACATTCGTGCGGAGCGTGACATTCTAGTGGAGGCAGACAGTT 722
                                                                                                                                                                                    GCTTTATCCACCGGGACATCAAGCCTGACAACATACTCATCGACCTGGATGGTCATATTA
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Bushnell, Steven E.
Carroll III, Eddie
Catino, Theodore J.
Derti, Adnan
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Astle, Jon H.
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  TCGCTCCGGAGGTGCTTCTCCGCAAAGGGTACACGCAGCTCTGTGACTGGTGGAGCGTCG 2386
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                                            TTGCTCCTGAAGTTTTGCTGAAGAAAGGATATGGCATGGAATGTGATTGGTGGTCATTAG
                                                                                        GTGTGATTCTCTTTGAGATGCTGGTTGGGCAGCCGCCTTTCTTGGCCCCCCACCCCACAG
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; OTHER INFORMATION: Incyte ID No. US20020156263A1 347975.11
US-09-974-298-152
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APPLICANT: Cheh, Huei-Mei
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE: PA-0037 P
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Pred. No. 8.3e-51;
0; Mismatches 493;
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CURRENT FILING DATE: 2011-10-04
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 194
SEQ ID NO 152
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Patent No. US20020156263A1
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Matches 577; Conservative
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US-09-764-868-196
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SEQ. ID NO 1:96
                                 LENGTH: 734
                                                                      TYPE: DNA
                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11111 | 111111 | 11111 | 111 | 111 | 111 | 111 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1589 CTGGGCTCTGTGAGGCCGAGCAGGAGCAGATGAGGAAGATCCTCTACCAGAAGGAGTCTA
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF,SEO ID NOS: 1510
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                     TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION TITLE OF INVENTION: PRODUCTS
THE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/879,536
CURRENT FILING DATE: 2001-09-21
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Pred. No. 2.66
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. US20020168711A1
GENERAL INFORMATION:
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O
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Best Local Similarity 68.8%;
Matches 308; Conservative
                                                   Lewis, Marcia E.
Monahan, John E.
                                                                                                                          Schlegel, Robert
                  Ford, Donna M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1)...(678)
; OTHER INFORMATION: n .
US-09-879-536-66
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SOFTWARE: Fasc
SEQ ID NO 66
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                                                                            1747 AAGCTGGACACTCACGCTCTGTACGCCATGAAGACTCTCAGGAAGAAGGATGTCCTGAAC 1806
                                                                                                                                                                                                                                    1867 IGGGIGGICAAACICIACIACITCCAGGACAAGGACAGCCIGTACIIIGIGAIGGAC 1926
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                                                                                                                                                                                1987 CIGGCCCGCTICIACAIIGCAGAGIIGACCCIGGCCAIIGAAAGIGICCACAAGAIGGGC
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                                         36;
Length 734;
                                         Indels
Score 192.2; DB 9;
Pred. No. 2.9e-42;
1; Mismatches: 294;
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TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REPERBNCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
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SEQ ID NO 369.
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                                                                                                                                                                                                                                                                                                                      DB 10; Length 1818;
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APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 271;
                                                                                                                                                                                                                                                                                                                                             7e-36;
                                                                                                                                                                                                                                                                                                                    5.4%; Score 169.4; ilarity 55.8%; Pred. No. 7.7 Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR PAPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-6-15
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PATENTIN VETSION 3.0
SEQ ID NO 89
LENGTH: 1818
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Scherf, Uwe
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                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-09-771-161A-89
                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 343; Conserv
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                                                                                                                                                                                                                              TYPE: DNA
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1689 GTTTGTGAAAATCAAGACTCTAGGCATCGGTGCCTTTGGGGAAGTGTGCCCTCGCTTGTAA 1748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATACCAGGGGGGTATGATGAGCCTGCTGATCAGGATGGAGGTCTTCCCTGAGCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1989 GGCCCGCTTCTACATTGCAGAGTTGACCCTGGCCATTGAAAGTGTCCACAAGATGGGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2549;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 161.8; DB 10; Length
Pred. No. 1.1e-33;
0; Mismatches 182; Indels
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR PLING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PALENTIN Ver: 2.1
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PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (1)..(2549)
; OTHER INFORMATION: n = a.or c or g or
US-09-880-107-3691
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59.88;
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Scherf, Uwe
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Best Local Similarity 59.8%
Matches 271; Conservative
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                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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GGCCGAGCAGGAGCAGATGAGGAAGATCCTCTACCAGAAGGAGTCTAACTACAACCGGCT 1661

Indels

pred. No. 2.3e-30;
0; Mismatches 227;

ilarity 56.5%; Conservative

Best Local Similarity Matches 299; Conserv

1602

899

1662

GCCCCAGGACAAGTACGTGGCCGACTTCTTGCAGTGGGCGGAGCCCATCGTGGTGAGGCT

GAAGAGGGCCAAGATGGACAAGTCCATGTTGTGAAAATCAAGACTCTAGGCATCGGTGC 1721

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2060 ACATCAAGCCTGACAACATACTCATCGACCTGGATGGTCATATTAAGCTGACAGATTTTG 2119
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                                                                                                                                                                                                                                                             1700 TCAAGACTCTAGGCATCGGTGCCTTTGGGGAAGTGTGCCTCGCTTGTAAGCTGGACACTC 1759
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                                                                                                                                                                                                                                                                                       1940 GGGATATGATGAGCCTGCTGATCAGGATGGAGGTCTTCCCTGAGCACCTGGCCCGCTTCT
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Pred. No. 4e-32;
0; Mismatches 179; Indels 0;
                                                                                                                                   ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M34182
US-09-880-107-2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: YOGANATHAN, THILLAINATHAN
TITLE OF INVENTION: DYSTROPHIA MYOTOWICA PROTEIN KINASE
TITLE OF INVENTION: DW-PK) AND ITS USES
FILE REFERENCE: KINEO22CON
CURRENT APPLICATION NUMBER: US/09/971,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1 LENGTH: 3407 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: PCT/US01/21479
PRIOR FILING DATE: 2001-09-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/238,558 PRIOR FILING DATE: 2000-10-04
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Patent No. US20020132247A1
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                                                                                                                                                                                               Query Match,
Best Local Similarity 59.5%;
Matches 263; Conservative
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID.NOS: 3950
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2340
LENGTH: 1635
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US-09-971-845-1
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                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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US-09-971-845-1
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Length 3407;

4.7%; Score 149.8; DB 10;

Query Match

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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT APPLICATION NUMBER: US/09/938,842A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1259 CAAGITIGGGGAGCGGATICCGGCCGAGAIGGCGCGCTICIACCIGGCGGAGAIIGICAI 1318
                                                                                                                                                                                                                                                                                                                                                                2019 GGCCATIGAAÀTGICCACAAGAIGGGCTTTAICCACCGGGACAICAAGCCIGACAACAI 2078
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                                                                                                   TCTCAGGAAGAAGGATGTCCTGAACCGGAATCAAGTGGCCCCATGTCAAGGCTGAGAGGA
                                                                                                                                                                                   1902 GGACAGCCTGTACTTTGTCATGGACTACCAGGCGGGGGATATGATGAGGCCTGCTGAT
                                                                                                                                                                                                                                                                                                 CAGGAT----GGAGGTCTTCCCTGAGCACCTGGCCCGCTTCTACATTGCAGAGTTGACCCT
                                    CTTTGGGGAAAGTGTGCCTCGCTTGTAAGCTGGACACTCACGCTCTGTACGCCATGAAGAC
Length 1398;
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Pred. No. 1.8e-28;
0; Mismatches 190;
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PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-10-16
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
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Best Local Similarity 57.4%;
Matches 256; Conservative C
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SEQ ID NO 633
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US-09-938-842A-633
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                                                                                                                                                                                                                                                                               2050 ATCCACCGGGACATCAAGCCTGACAACATACTCGACCTGGATGGTCATATTAAGCTG 2109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297 ITTGAAATAATTAAAGTAATTGGAAGAGGTGCTTTTGGTGAGGTTGCTGTTGTCAAAATG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  718 GCTCGTGTGTACACTGCAGAAATCGTCTCTGCAGTTTCCCATCTCCATGAGAAAGGCATA 777
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                          1870 GIGGICAAACTCTACTACTCCTTCCAGGACAAGGACAGCCTGTACTTTGTGATGGACTAC
                                                                                                                                      ATACCAGGCGGGGATATGATGAGCCTGCTGATCAGGATGGAGGTCTTCCCTGAGCACCTG
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2; Mismatches 176;
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                                                                                                                                                                                                                                                                                                                                                                 2110 ACAGATTTTGGCCTCTGCACTGGATT 2135
                                                                                                                                                                                                                                                                                                                                                                                            838 ACTGATTTTGGTTTAGCAAAAGAATT 863
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Best Local Similarity 58.3%;
Matches 253; Conservative
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US-09-764-868-58
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LENGTH: 17.35
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                                                                                                                                                                                                                                                                                                 ATACCAGGCGGGGATATGATGAGCCTGCTGATCAGGATGGAGGTCTTCCCTGAGCACCTG 1989
                                                                                                                                                                                                                                                                                                                                                                                   GCCCGCTTCTACATTGCAGAGTTGACCCTGGCCATTGAAAGTGTCCACAAGATGGGCTTT 2049
                                                                                                                           AATCAAGTGGCCCATGTCAAGGCTGAGAGGGACATCCTGGCTGAAGCAGAATGAGTGG 1869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCCACCGGGACATCAAGCCTGACAACATACTCATCGACCTGGATGGTCATATTAAGCTG 2109
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                                                                    478 AAAGACACGTCTGAGATATACGCGATGAAGGTCATGAGAAAAGATAAAATTGTTGAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-08-24 PRIOR APPLICATION NUMBER: US 60/264,647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2503, Application US/09938842A Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2110 ACAGATTTTGGCCTCTGCACTGGATT 2135
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SEQ ID NO 2503,
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APPLICANT: Harper, Jeff
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Zhu, Tong
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US-09-938-842A-2503
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Search completed: January 16, 2003, 22:04:38 Job time: 144.552 secs

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BI412714.1 GI:15173637
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                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
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JOURNAL
COMMENT
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KEYWORDS
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                                                                                    be, found
                                                                          Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: TRAK Plate: 54 Row: m Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7657294
This clone has the following problem: no polyA-tail
                             X., Hulyk, S.W., Hale, S.M.,
S., Martin, R.G., Muzny, D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCCTGCCTTTTGCCAACGAGTCAGGCACTTCGGCAGCTGCAGGTGAACCGGCAGATG 120
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                                                                                                                                                                                                                         /tissue_type="Eye, retina, mouse strain C57Bl\6"
/clone_lib="NIH_MGC_94"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                         DB 11; Length 1547;
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                     8e-223;
                                                                                                                                                                                                                                                                                                                      Score 927.6; I
Pred. No. 1.8e-
0; Mismatches
                                                                                                                                                                                                                                                                   /note="Vector: pcMV-SPORT6"
468 c 446 g 283 t
                          Gunaratne, P.H., Garria, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                    /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:5360539"
                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                      29.4%;
illarity 99.6%;
Conservative
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ORIGIN
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1353 row: n column: 09
High quality sequence start: 4
High quality sequence stop: 858.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B1412714 926 bp mRNA linear EST 14-AUG-2001 602987439F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5143496 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 926)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. " 287 c 272 g 166 t
1454 TTGTACGAGCTGGGCTCCACGGTGCCCTGGTCTGCAGCTCCACTGGCACGCGGGACTCG 1513
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                                                                                    GCGGCTACCCCACCTGGGGCCCACCCATTACATGTGTTGGGCACCCGGGGTCCCACGTTT
                                                                                                                  1334 GCGCTACCCACCTGGGCCCACCATACATGTTTGGGCACCGGGGTCCCACGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: M. Bento Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="InAGE:5141496"
/clone=lib="NCI_CGAP_Lu33"
/tissue_type="pooled lung tumors"
/lab_host="DH10B (phage-resistant)"
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Pred. No. 9e-187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Robert Strausherg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
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Eukaryota; Metazoa; Chordata; Craniata;
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BQ9304 EST.	nouse mouse. NISM Mus musculus Eukaryota; Metazoa; Chordata;		AL O	cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be	found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM13995 row: 1 column: 05 High quality sequence stop: 554.	rce	-res	/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally; oligo-dr primed. Average insert size 3 3 kb. Library enriched for full-length clones and constructed by Life Technologies.	OUNT 230 a	Ouery Match 24.8%; Score 781; DB 14; Length 924; Best Local Similarity 99.3%; Pred. No. 1.8e-186; Matches 795; Conservative 0; Mismatches 5; Indels 1; Gaps 1	2354 GGTACACGCAGCTCTGTGACTGGTGGAGCGTCGTGTGATTCTCTTTGAGATGCTGGTTG 2413 	2414 GGCAGCCGCCTTTCTTGGCCCCCCACACAGAGACGCAGCTGAAGGTGATCAACTGGG 2473 	2474 AGAGCACGCIGCAFATCCCTACGCAGGTGAGGCTCACGCGCTGAGGCCCGAGACCTCATCA 2533 	2534 CGAAGCTGTGCTGCGGGTGACTGCCGCCTGGCCAGGATGGGGCAGATGACCTCAAGG12593 	2594 CACACCGTICTICAACACCAICGACITITCCCGIGACAICGAAAGCAGGCIGCACCCI 2653 	2654 ACGICCCCACCATCAGCCCCCATGGACACCTCCAAITTTGACCCGGTGGATGAAGAAA 2713 	2714 GCCCTGGCACGAGGCGAGAGAGACCCAAGGCCTGGGACACGCTGGCCTCCCCA 2773 	2774 GCAGCAAGCATCCAGAGCACCCTTCTATGAGTTCACCTTCCGCAGGTTCTTCGATGACA 2833 
VERSION	SOURCE ORGA	REFERENCE AUTHORS TITLE	JOURN	•		FEATURES sou			BASE C	Oue Bes Mat	Qy	Qy Db	Qy	Qy Dp	Oy Dp	Qy.	Qy Db	Qy Dh
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                                                                                                                                                                                                                                                                          TCAACACCATCGACTTTTCCCGTGACATCCGAAAGCAGGCTGCACCCT 2653
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                           1;
Length 924;
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24.8%; Score 781; DB 14;

y 99.3%; Pred. No. 1.8e-186;

rrvative 0; Mismatches 5;
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5', mRNA sequence. BQ930443

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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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ACGGCTATCCCTTCCGGTGCCCGAAGCCCTCAGAGCCCGCAGAGAGTGCAGACCCAGGGG 2893
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11822 row: b column: 14
High quality sequence stop: 798.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                  ATGCGGACTTGGAAGGTGCGGCCGAGGGCTGCCAGCCGGTGTACGTGTAAGCCTCAGTTA
                                                                                                      Contract: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/clone_lib="NCI_CGAP_Mam6"
/sex="female, virgln"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
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Pred. No. 3.3e-184;
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/strain="FVB/N"
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UI-M-EHOD-buu-b-12-0-UI.rl NIH_BMAP_EHOP Mus musculus cDNA clone IMAGE:5686955 5', mRNA sequence.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                               121 TTAAAGACCCTGGAGCAGCAGGGGCGCAGAAGCAGCACCAGAGGTGCCTGTT
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                                                                                                                                                                                                                                                                                                                     241 TGTGACTGGTGGAGCGTGTGTGATTCTCTTTGAGATGCTGGGTTGGGCAGCCGCTTTC
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                                           GACAGCATGGAGCCCGGTGACCTCTGGGACGATGTTTCCAACTGTCGCTGTGGAGACAGG
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	1970 AGGTCTTCCCTGAGCAGCTGGCCGCTTCTACATTGCAGAGTTGACCCTGGCCATTGAAA 2029	BB354465 BB354465 BB354465 BB354465 BB354465  WENCALULS CONA Clone B930098K05 3', mRNA sequence. BB354465.2 GI:16405621 EST. HOUSE mouse. MUS musculus EURAryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleos Manmalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae	Hiramoto,K. Hiramoto,K. M., Koya,S., Okazaki,Y., Okazaki,Y., Tagami,M., Te	Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTS (Arakawa, T., et al. 2001) AL Unpublished (2001) On Jul 12, 2000 this sequence version replaced g1:9066293. Contact: Yoshinide Hayashizaki Laboratorry for Genome Exploration Research Group, RIKEN GE Sciences Center (GSC), Yokohama Institute	The Institute of Physical and Chemical Research (RIKEN) 17-22 Suchino-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japai 181-45-503-9222 Fax: 81-45-503-9216 Email: genome-reseggc.riken.go.jp, URL:http://genome.goc.riken.go.jp/ Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itol	Hayash er-sele 1 disco 10) Izawa, (., Tan	RIKEN integrated sequence analysis (RISA) system384 format sequencing pipeline with 384 multicapillary sequencer. Genome Res 10 (11), 1757-1771 (2000) Konño, H., Fukunishi, Y., Shibata, K., Itch, M., Carninci, P., Sugaha, Y. and Hayashizaki, Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a
	0	RESULT 6 BB354465 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM		TITLE JOURNAL COMMENT			· · · · · · · · · · · · · · · · · · ·
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Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. James Lin, Univeristy of Iowa Tissue Procurement: Dr. James Lin, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of CDNA Sequencing by: Dr. M. Bento Soares, Univeristy of DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov This clone was contributed by the Brain Molecular Anatomy Pro	Seq primer: prx.5. Location/Qualifiers 1 737 / Organism="Mus musculus" //strain="C57BL/6" /db_xref="taxon:10090" //clone="lib="NIH_BMAP_EHOp" //tissue_type="whole brain" //tasue_type="mboryo 18.5 dpc" //lab_host="DalloB (T1 phage resistant)" //note="Organ: brain; Vector: pvx-Asc; Site_1: EcoR I;	Bonaldo, Lennon and Soares, Genome Research, 6:791-80 Bonaldo, Lennon and Soares, Genome Research, 6:791-80 1996. Denatured mRNa was size fractionated on a 1% agel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stratch cDNA was size selected according to mRNA size fractic cDNA was size selected according to mRNA size fractic ligated with EcoR I adaptor, digested with Not I, and cloned directionally into pry-Acc vector. The library sequence located between the Not I site and the polyfy is CAGCCACGAC. This library was created for the University of Iowa Mouse Brain Molecular. Anatomy Prof. (BMAP): 'Gene Discovery in the Developing Mouse Nerve System', supported by National Institute of Mental H (NIMH), Hemin Chin, Ph.D., program coordinator."	tch al Similari 736; Cons	CGAAGGGAGACAAAGGCAGAGACAAAAAGCAGTTCAGACCTCCCCGGTGCCTGTCC         142           HILLIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	GCAAGAATAGCAGAGATGAAGAGAAGAGAGTCTCGCATCAAGAGTTACTCCCC CCTTCAAATTCTTCATGGAGCAACACGTGGAGAAATGTCATCAAAACCTACCAGCA [	TCAGCCGGAGGCTACAGCTGGAGCAGGAAATGGCCAAAGCTGGGCTCTGTGAGGCAGCCGCGCGCTCTGTGAGGCAGCCGGCCTCTGTGAGGCCAAAGCTGGGCTCTGTGAGGCCTACCGGACTCAACTACTACTACAACGCTGAAAGGACGTCTAACTACAACCGGCTCAACTAACT	300 CCAAGATGGACAAGTCCATGTTTGTGAAAATCAAGACTCTAGGCATCGGTGCCTTTGGGG 359 1730. AAGTGTGCCTCGCTTGTAAGCTGGACACTCACGCTCTAGGCATCGGTGCCTTTGGG 359 1730. AAGTGTGCCTCGCTTGTAAGCTGGACACTCACGCTGTACGCCATGAAGACTCTCAGGA 1789 11111111111111111111111111111111111
JOURNAL	FEATURES		ORIGIN Query Ma Best Loc Matches	1370	61 1490 121 1550	180 1610 240 1670	3 3

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54465 RIKEN full-length enriched, 10 days neonate cerebellum Musculus cDNA clone B930098K05 3', mRNA sequence.
54465.2 GI:16405621
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iramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
, Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
zaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sassaki, Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
ami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
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ublished (2001)
Jul 12, 2000 this sequence version replaced g1:9066293.
tact: Yoshihide Hayashizaki
tact: Yoshihide Hayashizaki
toratory for Genome Exploration Research Group, RIKEN Genomic
ences Center(GSC), Yokohama Institute
ences Center(GSC), Yokohama Institute
Institute of Physical and Chemical Research (RIKEN)
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.Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
.Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
.Konno,H., Okazaki,Y., Muramatsu,M., Isanaka,M., Ohara,E.,
.Rawai,J., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
.Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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nalia; Eutheria;
(bases 1 to 687)
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Sugahara

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., Aizawa
                                                                                                                                                                     cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGAGAGAGGATCCAAGAGCTCTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
                                                                                  Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RIKEN full-length enriched, 10 days neonate cerebellum"
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  edundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) 10,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Al: Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2449 ACGCAGCTGAAGGTGATCAACTGGGAGAGCACGCTGCATATCCCTACGCAGGTGAGGCTC 2508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 GCCTGGGACACGCTGCCCCCCAGCAGCAACCACCAGAGCACCCTTCTATGAGTTC
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Pred. No. 7.4e-156;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="10 days neonate"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="cerebellum"
                                                                                                                                                                                                                                                                                                                             /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                               /strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                          prepare mouse tissues.
Location/Qualifiers
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cDNA library.
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                                                                                                                                                      further details.
                                                                Hayashizaki, Y.
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AGENCOURT_8489599 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:6180847 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5'-TCGACCCCACGCGTCG-3' and 5'-TCGACCCACGCCGTCG5'-3'. Size selected > 5'-GATGGTTGTAGATGCGACCGCCCCCT(15)-3'. Size selected > 1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
Not1; Site_2: Sal1; cDNA made by oligo-dr priming.
Directionally cloned using the following adaptors:
                                                                                                                                                                                                                                                                          3047
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                                                                                                                                  481
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                                                                                                                                                                                                                                                                                                                    601
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 930)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                            ACCTTCCGCAGGTTCTTCGATGACAACGGCTATCCCTTCCGGTGCCCGAAGCCCTCAGAG
                                                                                                                                                                                                     ACCTTCCGCAGGTTCTTCGATGACAACGGCTATCCCTTCCGGTGCCCGGAGCCCTCAGAG
                                                                                       CCCGCAGAGAGTGCAGACCCAGGGGATGCGGACTTGGAAGGTGCGGCCGAGGGCTGCCAG
                                                                                                                                     CCCGCAGAGAGTGCAGACCCAGGGGATGCGGACTTGGAAGGTGCGGCCGAGGGCTGCCAG
                                                                                                                                                                                    CCGGTGTACGTGTAAGCCTCAGTTAACCACAACTCGAGGAAACCCAAAATGAGATTTCTŢ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:6180847"
/clone_lib="Lupski_dorsal_root_ganglion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://image.llnl.gov
Plate: LLAM13564 row: e column:
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/db_xref="taxon:9606"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            3108 ATTTTTTAAAAATTAGTACAGTATGG 3134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
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AUTHORS
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KEYWORDS
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GGCTACAGCTGGAGCAGGAAATGGCCAAAGCTGGGCTCTGTGAGGCCGAGCAGGAGCAGA 1618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1679 ACAAGTCCATGTTTGTGAAAATCAAGACTCTAGGCATCGGTGCCTTTGGGGAAGTGTGCC 1738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCGCTTGTAAGCTGGACACTCACGCTCTGTACGCCATGAAGACTCTCAGGAAGAAGGATG 1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1799 TCCTGAACCGGAATCAAGTGGCCCATGTCAAGGCTGAGAGGGACATCCTGGCTGAAGCAG 1858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 TCTTCATGGAGCAACACGTGGAGAATGTCATCAAAACCTACCAGCAGAAGGTCAGCCGGA 190
                                                                    NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: liver, Vector: pcMV-SPORT6. Site_1:
Site_2: SalI; Cloned unidirectionally. Primer: Oli
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCGCTTGTAAGCTGGACACTCACGCTCTGTACGCCATGAAGACTCTCAGGAAGAAGGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1384 GCTGGCAGAGACAAAAAGCAGATTCAGACCTCCCCGGTGCCTGTCCGCAAGAATA--
                   Craniata; Vertebrata; E
Sciuroqnathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="INAGE:5135667"
/clone_lib="NCI_CGAP_Li9"
/lab_host="DH10B (T1 phage_resistant)"
                                                                                                                                                                                                                          DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution i
found through the I.M.A.G.E. Consortium/Linn
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 622; DB 13;
Pred. No. 2.7e-146;
N. Mismatches 15;
                   Craniáta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 2.7e
0; Mismatches
                                                                                                                                                                                                                                                                                                   Plate: LLAM11333 row: h column:
High quality sequence stop: 683.
Location/Qualifiers
                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
                 Chordata;
                                       Rodentia;
                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.78;
97.08;
                     Eukaryota; Metazoa;
                                     Mammalia; Eutheria;
                                                         (bases 1 to 689)
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les 656;
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AUTHORS
TITLE
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us cDNA clone IMAGE:5135667 5',
                                                                                                                               ACAAGAGCCACAAAGGTGCGAAGGGAGACAAAGCTGGCAGAGACAAAAAGCAGATTCAGA 1411
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                                                                                                                                                                                                                                                                                                                                                          AAACCTACCAGCAGAAGGTCAGCGGAGGCTACAGCTGGAGCAGGAAATGGCCAAAAGCTG 1591
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                                                                                                                                                                                                          AGAGTTACTCCCCTTATGCCTTCAAATTCTTCÀTGGAGCAACACGTGGAGAATGTCATCA .1531
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                                                       14;
                                                                                          0; Mismatches 101;
                                                     637.4; DB
No. 4e-150;
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Mus musculus
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B1331257
B1331257.1 GI:15015901
                                                     20.2%;
 U
                                                                                            Conservative
229
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1558

130

310

250

-G 1439

Gaps

5,

Indels

1918

550

490

DEFINITION

RESULT 8 BI331257

ACCESSION VERSION KEYWORDS SOURCE

us-09-763-334-5.rst

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discovery
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BE986745/c
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MEDLINE
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Clone distribution: NCI-CGAP clone distribution information can be
flound through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM11159 row: n column: 16
High quality sequence start: 10
High quality sequence storp: 745.
                                                                                                                                                                                              BI525737 824 bp mRNA linear EST 29-AUG-2001 602926563F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5059023 5',
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                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I t bases 1 to 824)
II + MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
TGATGGACTACATACCAGGCGGGGATATGATGAGCCTGCTGATCAGGATGGAGGTCTTCC 1978
                                                   CTGAGCACCTGGCCCGCTTCTACATTGCAGAGTTGACCCTGGCCATTGAAAGTGTCCACA 2038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTTGGGGAAGTGTGCCTCGCTTGTAAGCTGGACA-----CTCACGCTCTGTACGCCATG 1776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1777 AAG--ACTCTCAGGAAGAAGGATGTCCTGAACCGGAATCAAGTGGCCCCAT--GTCAAGGC 1832
                                                                 824 CTTTGGGGAAGTGCCCCTCGCTTTGTAACCTGGGACACTGCACGCTTCTGGTACGCCATG 765
                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                         TGATGGACTACATACCAGGCGGGGATATGATGAGCCTGCTGATCAGGATGGAGGTCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                            Bonaldo, Ph.D. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism "Mus musculus"
                                                                                                                                                                                                                                               BI525737.1 GI:15350529
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ilarity 94.3%;
Conservative
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BI525737
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BI525737/c
LOCUS
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                                                                                                                               671
                                                                                                                                                                                                       DEFINITION
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575 bp mRNA linear EST 29-APR-2002 UI-M-CGOp-bey-c-06-0-UI.sl NIH_BMAP_Ret4_S2 Mus musculus cDNA clone BE986745
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 575)
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Normalization and subtraction: two approaches to facilitate
                           CTGGATTCAGGTGGACTCACAATTCCAAGTACTACCAGAAAGGGAACCACATGAGACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     285 TAAAGA -CCTGGAGCAGAGAGGCGCAGAAAGCAGCACCAGAGGTGCCTGGCACATTCTCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 GTGACTGGTGGAGCGTCGGTGGATTCTCTTTGAGATGCTGGTT-GGCAGCCGCCTTTCT
TGAGAGGGACATCCTGGCTGAAGCAGACAAT-GAGTGGGTGGTCAAACTC-TACTACTCC
                                                                                                                                                                                               GAGCCTGCTGATCAGGATGGAGGTCTTCCCTGAGCACCTGGCCCCGCTTCTACATTGCAGA
                                                                                                                                                                                                                                                                                        2010 -GTTGACCCTGGCCATTGAAAGTGTCCACAAGATGGGCTTTATCCACGGGACATCAAGC
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6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
20892-9643, USA
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Fax: 301 443 9890
Email: mEST@mail.nih.gov
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Oligo dr track not found, Not I site shown in beginning of sequence is likely internal to the message. CDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain. BMAP CDNA colones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP CDNAs whose availability will be considered under appropriate and limited collaborative arrangements The tissue for this library was contributed by Dr. Xin-Yuan Fu, Seq primer: Ml3 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   various stages of development. For a detailed description of the library from which this clone was derived, please visit our web site at brainest.eng.ulowa.edu. The tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for this library was contributed by Dr. Xin-Yuan Fu, Yale University School of Medicine TAG_SEQ=None found" 10 t 163 c 200 g 110 t
                                                                                                                                                                                                                                                                                                                                                              /lab_lost="DHIOB (Life Technologies)" with a modified /note="Vector: pT7T3D-Pac (Pharmacia).with a modified polylinker, Site=1: Not I. Site_2: Eco RI; The NIH, BMAP.Ret4_52 library is a subtracted library, ultimately derived from mouse retina tissue libraries at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358 TACCACCAGCTGGGTGGTGCAAACTACGAGGGCCCCGCCGCACTGGAGGAGATGCCGCGG 417
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Pred. No. 3e-131;
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Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
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/lab_host="DHIOB (Life Technologies)"
/note="Vector: pr77B0-pac (Pharmacia) with a modified
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Mammalia; Butheria; Rodentia; Sciurognathi; Muriand
Jonalda war
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Pred. No. 4.6e-129;
0; Mismatches 2;
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/clone="UI-M-CG0p-bms-a-06-0-UI"
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University School of Medicine
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/organism="Mus musculus"
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ilarity 99.5%;
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Eukaryota; Metazoa;
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Fax: 301 443 9890
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/note="vector: pr710-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The Note="vector: pr710-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The Note="vector: pr710-Pac (Site_2: Eco RI; The Utimately derived from a mixture of individually tagged ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hipoccampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated in this process: NIH_BMAP_M.S3. in NIH_BMAP_M.S3. vill_BMAP_M.S3. vill_STANDAMS.SA. vill_STANDAMS.SA. vill_STANDAMS.SA. vill_STANDAMS.SA. vill_STANDAMS.SA. vill_STANDAMS.SA. vill_STANDAMS.SA. vill_STANDAMS.SA. vill_STANDAMS.S
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0; Mismatches 6;
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181 c 16
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Best Local Similarity 98.9%;
Matches 543; Conservative
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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449 TCCCAAAGGGTACAGCACAGCAGTAGAGCCCAAGTGCGCACTTTCCGGGCACACACTATGG 390
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                                                                                                                                                                                                                                 1329 GAACAGACGCCACCAGAFGCCTATTCCAGCATGGCCCAGGGCCCAGGGTGGCCTCCCGC
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                                                                 606 GAACAAGACGCCACCAGATGCCTATTCCAGCATGGCCAAGGCCCAGGGTGGCCCTCCCGC
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DEFINITION

RESULT 12

AW494954

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE

MEDLINE

JOURNAL

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Oligo-dr track not found, Not I site shown in beginning of sequence is likely internal to the message. CDNA Library Preparation: M. B. Soares Lab Clone distribution: Researchers may obtain BMAP CDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP CDNAs whose availability will be considered under appropriate and limited collaborative arrangements Seg primer: M13 Forward
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Normalization and subtraction: two approaches to facilitate gene
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/lab_host="DH108 (life Technologies)"
/note="vector: pT7730-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The
                                                                   816 GTCCAGGAACAGCCTCAATGCTGACTTGTACGAGCTGGGCTCCACGGTGCCCTGGTCTGC 875
       Sciurognathi; Muridae; Murinae;
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National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
60892-9643, USA
Tel: 301 443 1706
Fex: 301 443 9890
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                         cDNA clone
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TAG_SGD=None found"

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                                                                                                                                                                                                                                                                                                                                                                             Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pr/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: ECO RI; The NIH_BMAP_Ret4_S2 library is a subtracted library, ultimately derived from mouse retina tissue libraries at
                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 539)

Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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                                                                                                                                                                     UI-M-CGOp-bgr-g-12-0-UI.sl NIH_BMAP_Ret4_S2 Mus
UI-M-CGOp-bgr-g-12-0-UI 3', mRNA sequence.
BF465780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="UI M-CG0-bgr-g-12-0-UI"
/clone_lib="NIH_BMAP_Ret4_S2"
/lab_host="DH10B (Life Technologies)"
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Pred. No. 6.3e-125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
                                                                                                                                                              539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mEST@mail.nih.gov
                                                                                                                                                                                                                                                       BF465780.1 GI:11534963
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99.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 301 443 1706
Fax: 301 443 9890
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1468 ATCAAGAGT 1476
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BF465780/c
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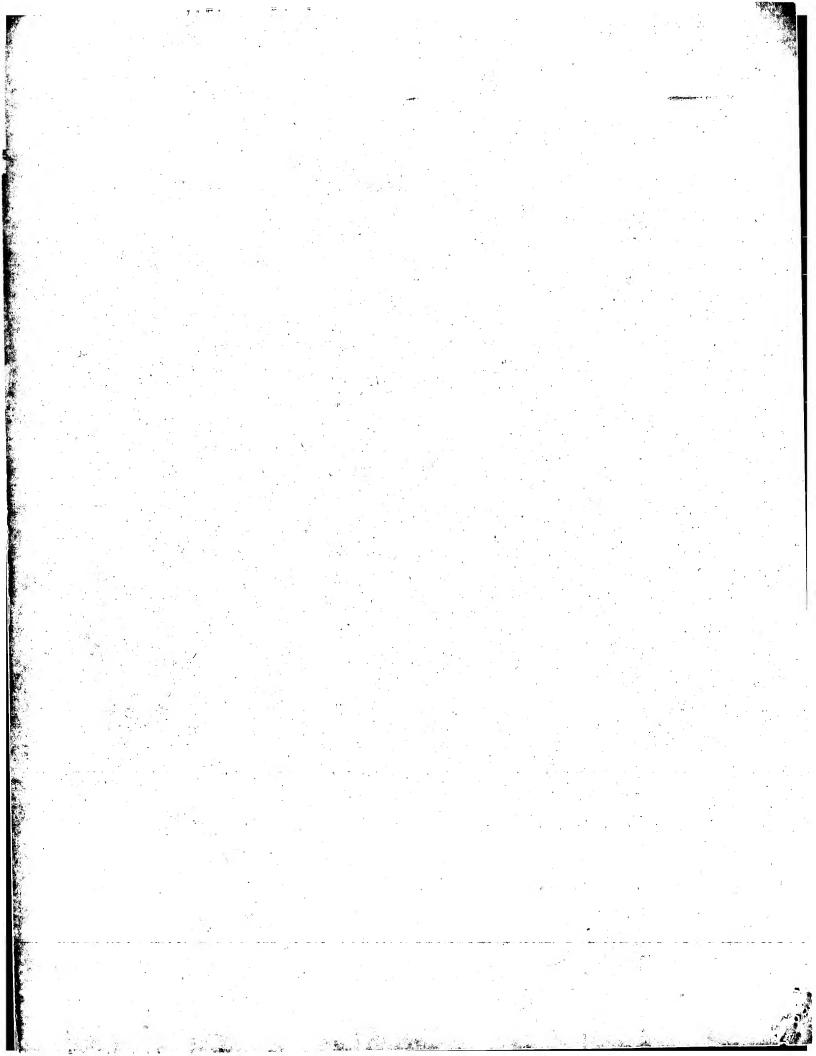
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Query Match
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                                                                                                                                                                                   perpresentation of the process in the BMAP_M_S4, were generated in this process in INL BMAP_M_S4, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1, NIH_BMAP_M_S4.2, NIH_BMAP_M_S4.3, NIH_BMAP_M_S4.3, NIH_BMAP_M_S4.3, NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.3, NIH_MS3.3, NIH_MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           into DH10B bacteria (LifeTechnologies) to generate the NIH, BMAP, M.S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
NIH BWAP M. S4 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, offactory bulbs, hypothalamus, cortex, amygdala, basal gandlia, pineal gland, striatum, hipoccampus) after a series of subtractions to reduce the representation of CDNAs from which ESTs had already been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated
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Pred. No. 5.1e-124;
0; Mismatches 2;
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TAG_LIB-NIH_BMAP_M_S4
TAG_TISSUB=corpus-striatum
TAG_SEQ-ACGCC"
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ilarity 99.6%;
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RESULT 15 BE620135

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BE620135 863 bp mRNA linear EST 20-OCT-2000
601483053Fl NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3885780 5',
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                                                                                                                                                                                           Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="large_cell carcinoma, undifferentiated"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 2.8e-120;
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Primates; Catarrhini
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
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AR201456 Sequence AF104414 Mus muscu AR201455 Sequence AR201454 Sequence L39837 Drosophila AC007821 Drosophil AE003775 Drosophil AC012975 Drosophil AC012900 Drosophil AB023958 Mus muscu BC009658 M**ūs** muscu Drosophil Drosophil Drosophil Drosophil AF239171 Drosophil AC102227 Mus muscu E38226 Human tumor E38227 Human tumor 224613 warts Prote warts Prote AC098623 Rattus no AL356285 Human DNA Mus muscu L583963 Human DNA D.melanogas AR170696 Sequence X97657 N.crassa mR AB028019 Homo sapi AF207547 Homo sapi AF164041 Homo sapi AF104413 Homo sapi AC087136 Mus muscu Ustilago A52135 Sequence 1 AR084688 Sequence Sequence 6 AR084691 Seguence 235102 H.sapiens 3C012085 Homo sap 330329 M.crystall השתלביטוט (אמר 23-JUL-19 באימים) באימים דרמוז (ברמוז (ברמוז באימים באימים) באימים U29608 Drosophila AR201457 Sequence AR139101 Sequence AX056364 Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 5720) Xu,T., Wang,W., Zhang,S., Stewart,R.A. and Yu,W. ALIGNMENTS SUMMARIES DMU29608 Drosophila melanogaster. DB U29608.1 GI:903941 Length .8 2114 .6 215989 .6 2101 24506 18359 Query 99.8 99.8 91.2 Score REFERENCE AUTHORS

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	1 CGTCAAACTGAAGCCCATTGGAGTGGGTGCATTTGGCGAGGTAACGCTGGTGAGCAAAAT	1 CGATACCTCGAACCATTTGTATGCGATGAAAACCCTGCGGAAAGCGGACGTTCTCAAGCG	GAATCAGGTGGCACACGTGAAGGCCGAGAGGGATATCCTCGCGGAAGCCGACAATAACTC 	1 GGTGGTGAAGTTGTACTACAGCTTCCAGGACAAGGATAATCTGTÄCTTTGTGATGACTA 	1 CATACCAGGTGGTGATCTGATGTCGCTGCTGCATCAACTGGGCATTTTCGAGGAGGAACT 	1 GGCCAGATTCTACATCGCCGAGGTCACCTGCGCCGTGGACAGGGTTCACAAAATGGGCTT	L CATTCACAGAGACATCAAGCCTGACAACATACTCATCGATAGGGACGGAC	CACCGACTITGGCCTGTGCACGGGATTCCGATGGACGCACAACTCGAAGTACTACCAGGA	1 GAACGGCAATCACTCGCGCCAGGACTCGATGGAGCCCTGGGAGGAATACTCCGAGAACGG	ACCGAAGCCCACCGTGCTGGAGAGGCGACGGATGCGCGATCACCAAAGAGTCCTGGCCCA	1 CTCGCTGGTGGCCACCCCGAACTACATAGCTCCCGAGGTGCTGGAGGAGRAGTGGGTACAC	1 GCAGCTGTGCGACTACTGGACGTGGGCGTCATCCTYTAYGAGATGCTGGTGGTGGTCAGCC	1 GCCCTTTCTGGCCAACAGTCCGCTGGAAACGCAACAAAGGTCATCAACTGGGAGAAAAC 	1 SCTGCATATTCCGCCGCAGGCCGAGTTATCCCGCGAGGCTACGGACTTGATAAGGAGGCT 	1 CTGTGCGTCGGCTGACAAGCGGCTGGGCAAGAGCGTGGACGACGACGACGACGACTT	1 CTTCAAGGGCATCGACTTTGCGGACATGCGGAAGCAGAAAAGGCCCCTACATACCGGAAAT	CAAGCACCCRACGGACACATCCAACTTTGATCCCGTGGATCCGGAGAAGCTGCGCTCGAA	TGACTCCACCATGAGCAGGGGGGATGATGTCGACCAGAATGACGGCACYTTCCACGGCTT 
	324	330	336	342	3481	354	3601	3661	3721	378:	384	390:	396: 3961	402]	4081	4141	4201	4261
	Qy Db	Qy Dp	Qy Db	oy Ob	Oy Dp	Qy Db	9. Pb	O D	Q D	OY Db	Qy Dp	Oy Dp	oy D	Oy Op	oy Ob	Oy Dp	Qy Db	Oy Db

	Qy Db	4321	TTTCGAATTTACCTTCCGTCGCTTCTCGACGACAGCGGCCGCCGGATATGACGACGA 4	380
	Oy Db	4381	36CGCCGGTTTACGTCTGAAATGGATGCTCTCCATGTGCCCAACACCAACACCGGC 4-	4 4
	oy GD	4441	CCCCGAATCATTGTTAGTCAAATAGTCACAAAAAGGGGATAGAAACCATTGAGTGGGCTT 41	
	oy Db	4501	CATTATATAAATTATA 4 	
	oy Db	4561 4561	GGAGACAGTAGAGGCGGGAGCTACGTATATACATACAAATAATATACATATATTTGATAT 40	
	oy D	4621	SCATGAACTGAATAAATATAAAACGGAGCCGAGTAG 4	68
	oy Db	4681	AGATGAAACGAGGGGGGGGGTCAGGACCTTCGACCTTTAACTGAACATAGTATATCCTT 47	740
	Qy .	4741 4741	AACAAATATATATTTAAATTGTTAGAATTGAAAGGGRCCA 4	
	Oy Db	4801	ACTGGAAATCGAACCTTCTGGTGCTCAAAGCAAAGCAAA	960
	Qy Db	4861	TTAAACTAAAYGAGACGCGAATTTACCCAACCACTTCACTCCTCTCTCTTTCTCCACCTCC 49	920
	Oy Db	4921	GATCGGTGGCCGGATTCGAACTCAGCTGGTTGCATCCGGCCATCCCATTKACTTCC 45	086
	Oy Db	4981	SAGAACGAACGAGACCAAAAGTCGCAC 5	040
	VQ	5041	GGATATAAGCGGGTCTTATAAGCCTAATCTAAATCTAAACTGGGGAGAACAGGACC 5	100
	Qy	5101	CTATCACTGCTCTTCAWCTGWGTACGACCCCCAC 5	160 160,
	Qy	5161	GTAGCCTATGTGAAAAGCTAGCAAT 5	220
	Qy	5221	TTGTTGAATGCCAAATGAAATTGTTTAGCCCCACGAGGAAAACGCGGGG 5	280
•	Oy Dp	5281	TTCTCTGATAGCAAACGGAAAAGAAAGAAAGAAAAAAAAA	340
	Oy Dp	5341	GARACGAGAAAATTGTAATCTTCTTAATGTAATATTGTAAAGAACACGTTAATTGT 5	400
	QY.	5401	CCCTAAGATGTTTTAGTTTATAGACCGCTAACCG 5	460

Db 361 GAATCGGCTCAAATCAAATTAAAATCAACTAATATTTGGTATTCAGATATTCAAATGGTATTCGAATTGGTATTTCAAATGGTATTTGGTATTTTGAATTGGTATTTGAATTGGTATTTTGAATTTGAATTGGTATTTGAATTTGAATTGGTAATTGGTATTTGAATTTGAATTGGTAATTGAATTGGTAATTGAATTGGTAATTGGTAATTGAATTGA	Qy 481 GTGTCTGCGGCTGGCGCAGAATCTCTGATAAAGCAGAGGAATAAAATCGGAAGAACAACA	Oy 541 AATACAAATACAAATGAAATGCGGGGGGGGGGGGGTATTTACATGCCAAATGAATG	Qy 601 GCGAAAGGGGGGTTTCTCTTATAATGCAAATGTGAATGCGAATGCGAATGCGA 	OY 661 GTGGAAGAATTCCCGGCGCGAGTGATAAATAATCCGACGACAAACAA	QY 721 ACCGCGAGAAGAGCAGCACAACAATTATTGTTTATTGAGGCAACAATATCAGATC	QY 781 GAGATAATAAAGCATCCTAAAACCGGGGCCTTAGTTGTTYTAGTCTCGCCACRGATATA	OY 841 GATATTCAAAGGCAAAAAGGTGGTGTGCGCATCGCCAGACAAACAA	QY 901 TCATACAAAACAACCAATTAAATAATAAAAAAAAAAAA	OY 961 CAAATCAAATTCCCGGCCCGATGTCCCCCAGTGTGTGTGT	OY 1021 TGTGCTGTGCTGCGAGTGTTAGTGTGCGGAGCATTTCTGTGATATGAGTGCTAAATGC	OY 1081 CACAGGCGAAGCAGCACATCATGCATCCAGCGGGGGAAAAAGGGGCGGTCGCCCCAA	OY 1141 TGATAAATACACGGGGAAGCCTCGAGAGCATCAAGCAGCACCTAACCCGATTTGAAGT	Qy 1201 ACAAAATAACCATAGGAATAATCAGAATTACACACCTCTGGGATACACGGGGACCAAGGG	OY 1261 ACGCAACGATGCACTTACTCCTGACTATCACCCAGCCCAAGCAGGAGCCGCCCCCCCC	QY 1321 CTCCGCCTCCTGCTCCGGACGTGGTCATACCGCCGCCCGC	Oy 1381 CGGACCGGCTCCATATCCGTATCCGTGTGGCCGTTGGAGTGGTGGGTCTGGCGAACGG	
DD 5401 AATCTAGGTAGAGTTGTAGGGGCCCTAAGATGTTTTTAGTTTATAGACGGTAACCG 5460 Oy 5461 TAATCTAGTTTAATTCCTAACACTAAGGGAGTACAGTAC	 Qy       5521 GTAGGT/CGTTGGAAAATGCTTAACGGGAAACGATTGTTTTTCTCTTTAATTAGCTTCA       5580         DD       5521 GTAGGT/CGTTGGAAAATGCTTAACGGGAAACGATTGTTTTTCTCTTTAATTAGCTTCA       5580	OY 5581 GTTGTATGTGCGTGTGTTTTTATTATGACTTATATAGTCCATCTGAATATTGGGA 5640	OY 5641 TGGACCTATTTAAANGTGAGATGGACTAATTGAAGGAAATACAAACAAACTATGTT 5700 	Oy         5701         GCCTTGGCCAATTAGTTTAC         5720           Db         5701         GCCTTGGCCAATTAGTTTAC         5720	OC BAN	ITION Sequence 1 from patent US 6359193. SION AR201454 ON AR201454.1 GI:20252342	SOURCE Unknown. ORGANISM Unknown. Unclassified.	ADTHORS XU.T., Tao,W., Wang,W., Zhang,S. and Yu,W.  TITLE Nucleotide sequences of lats genes JORNAL Patent: US 635919-1 19-MAR-2002;	rce	Query Match 1 99.8%; Score 5708; DB 6; Length 5720; Best Local Similarity 99.5%; Pred No. 0; Matches 5693; Conservative 26; Mismatches 1; Indels 0; Gans 0;	SGACGACGCAGCAACAAAACCAGAATTAATTTTACTAAATTTAAGCAAACG 60 LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	C) C	121 GAGTGAATGAAGAGAAATAGGTGGGAAATATCAGGGAATTGTCGTCAAAAGGCAAGGA	181 AAAACGGAGAAAAAGGAAAAGCAATAAGTGCCGTGTGTGGGAAACGCGAAAAAGGA 24 181 AAAACGGAGAAAAAAAAAGAAAGAAAGCAAAAAGCGAAAAGGGAAAAGGGAAAAGGGAAAAGGGAAAAGGGAAAA	GAACAAAGGGCGAAAAGCGAGGAAATGCGTGGAAAACGTGGAAAACGGGAAGAAGGG 30	301 AGCTCCAAGTTGGCCGCCATGGATTCGTGYGTAGGATCAATTAAGATTCCGAGTGGTCGA 301 AGCTCCAAGTTGGCCGCCATGGATTCGTGYGTAGGATCAATTAAGATTCCGAGTGGTCGA 301 AGCTCCAAGTTGGCCGCATGGATTCGTGCGTCGATGAATTAAGATTAAGATTCCGATGGTCGA	THE PROPERTY OF THE PROPERTY O

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361   CACCRETTORCCTOTOCACCREGATTCCCRAGGACCCCACAACTCCAAATACTCCAAATACTCCACAACTACT	7,	4 4	Qy 4861 Db 4861	Oy 4921 Db 4921	Oy 4981 Db 4981	Oy 5041 Db 5041	Qy 5101 Db 5101	Qy 5161 Db 5161	Oy 5221 Db 5221	വ	Oy 5341 Db 5341		Oy 5461 Db 5461		Qy 5581 Db 5581		Oy 5701 Db 5701	RESULT 3 DROWARTS LOCUS DEFINITION	
161   CACCGARTTGGCCTGTGCACGGGATTCCATGGACCCACAACTCCAACTCCACACCCACACTCACACGGATTGGCCTGCACGCATTGGCCTGCACCACACCCACACTCCAACTCCACACGGATTGGCCTGCAACTCCACACGACCCCGACACTCCACACCCCACACTCCACACCCCCACACTCCACACCCCCACACTCCACACCCCCACACTCCACACCCCCACACTCCACACCCCCACACTCCACACCCCCACACTCCACACCCCCACACTCCACACCCCCACACTCCACACCCCCACACTCCACACCCCCACACTCCACACCCCCACACTCCACACCCCCACACTCCACACCCCCACACTCCACACCCCCACACTCCACCCCCACACTCCACACCCCCACACTCCACACCCCCACACTCCACACCCCCACACTCCACACCCCCACACTCCACACCCCCACACTCCACACCCCCACACTCACACTCACACACTCCACACTCCACACTCCACACTCCACACTCCACACTCCACACTCCACACTCCACACTCACACACTCCACACTCCACACTCCACACTCCACACTCCACACTCCACACTCCACACTCCACACTCACACACTCCACACTCACACTCCACACTCACACTCCACACTCACACTCCACACTCACACACTCACACTCACACTCACACTCACACACTCACACACTCACACACTCACACACTCACACTCACACACTCACACACTCACACACTCACACACTCACACACTCACACACTCACACACTCACACACTCACACACTCACACACTCACACACTCA	-			· .		· · ·	•				.*		· 	······································	· ·	•,			•
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Justice, W., Zillian, O., Woods, D.F., Noll, M. and Bryant, P.J.
The Drosophila tumor suppressor gene warts encodes a homolog of human myotonic dystrophy kinase and is required for the control of Genes Dev. 9 (5), 534-546 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        function="required for the control of cell shape and
                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                     homologue; myotonic dystrophy kinase; tumor suppressor gene.
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779 TCGAGATAATAAAGCATCCTAAAACCCGCGCCTTAGTTCGTTYTAGTCTCGCCACRGATA 838
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                                                                                                                                                                                                                                                                                        GAGTGAATCAAGTGAAAATACGTCGGCAAATATCAGCGAATTGTCGTCAAAAGGCAAGGA
                                                                                                                                                                               155 GAGTGAATCAAGTGAAAATACGTCGGCAAATATCACCGAATTGTCGTCAAAAGGCAAGGA
                                                                                                                                                                                                                        181 AAAACGGAGAAAAAAGGGAAAAGCAATAAGTGCCGTGTGTGGGAAACGCGAAAAAGGCGA
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                           17;
Length 5360;
                             Indels
  DB 3;
                             17;
 11.2%; Score 5216.4;
ilarity 98.9%; Pred. No. 0;
Conservative 26; Mismatches
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93	95	101	107	113	119	125	131	137	1439	149	1559	161	167	1739	179	185	1910	197
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.2552 2313 AGTGCCTCGGCCAGCAATTCACCAGTGCTGGCGGCGCTCCACCCTCTTACCCTCAG AGTGCCTCGGCCAGCAATTCACCAGTCCACGTGCTGGCCGCTCCACCCTCTTACCCTCAG 2673 GCTCAGAGGGAGCGGGATCAACGGGAGCGGGAACGGGATCAGCAGCAACGGA 2759 GAGATCAAACCGCCGAGCTGCAACAACAACATACAGATAAGCAACAGCAACCTGGCG 2793 GAGATCAAACCGCCGAGCTGCAACAACAACAATACAGATAAGCAACAGCAACAGCGCG 2193 AAGCCACAACCACGAGTCTACCAGGCCAGGAGTCAGCAGCAGCAGCAGCAGAGTGTG 2433 CATCAGCACCAGCAATCCAAACCAGCAACGCCCACCACACACGCCCTTGGTGGGGGGTCTGAAC AATCCTGGCCGGCAGATGCTTCCGCCGCCGCCCTATCAGAGCAACAACAACAACAACAGC 2733 AATCCTGGCCGGCAGATGCTTCCGCCGCCGCCCTAFCAGAGCAACAACAACAACAAGGC CATCAGCACCAGCAATCCAAACCACCAACGCCMACCACACGCCCTTGGTGGGTCTGAAY 2493 AGCAAGCCCAATTGCCTGGAGCCACCGTCCTATGCCAAGAGCATGCAGGCCAAGGCGGCC 2519 ACGCIGGTARAGCAGCAGCAGCAGCAGCAGCARCARCAGCAGGTCCAGCAGCAGCAG 2553 ACGGTGGTACAGCAGCAGCAGCAGCAGCAACAACAGCAGGTCCAGCAGCAGCAGGTG 2879 AGCTCGGGCGGCAGCAACGGATCCACCGGCACCACCGCCTCGTCGACCAGCTGCAAG 2013 GGAGGAGCACCGCCGCCGCCACCACCAGTTACACGGCCTCCATGCAGTCGCGGCAG **AAGCCACAACCACGAGTCTACCAGGCCAGGAGTCAGCAGCCGATCATCATGCAGAGTGTG** AAGAGCACGCAGGTCCAAAAAGCCCGTGCTGCAAACAGCAGTGGCGCGCCCAATCGCCATCG 2459 AGCAAGCCCAATTGCCTGGAGCCACCGTCCTATGCCAAGAGCATGCAGGCCAAGGCGGCC GCTCAGAGGGGAGCGGATCAACGGGAGCGGGAACGGGATCAGCAGAAGCTGGCCAACGGA 

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GCACAAAGTGGGACTGCCCGATCAGACCCAAATCGAGATGAGGAAAATG 	GGAGAGCAACTACATTCGATTGAAGGCGCCCAAGATGGACAAGAGCATG 	CTGAAGCCCATTGGAGTGGGTGCATTTGGCGAGGTAACGCTGGTGAGCAAA 	GAACCATTIGTATGCGATGAAACCCTGCGGAAAGCGGACGTTCTCAAG 	GGCACACGTGAAGGCCGAGAGGGATATCCTCGCGGAAGCCGACAATAAC 	AAGTIGTACTACAGCTICCAGGACAAGGATAATCTGTACTTTGTGATGGAC 	YTGGTGATCTGATGTCGCTGCTCATCAAACTGGGCATTTTCGAGGAGGAA 	CTACATCGCCGAGGTCACC 	GAGACATCAAGCCTGACAACATACTCATCGATAGGACGGAC	rescersescaes 	ATCACTCGCGCCAGGACTCGATGGAGCCCTGGGAGGAATACTCCGAGAAC	CCACCGTGCTGGAGAGGCGACGGATGCGCGATCACCAAAGAGTCCTGG 	TGGGCACCCCGAÂCTACATAGCTCCCGAGGTGCTGGAGAGRAGTGGGTAG 	GCGACTACT	CTGGCCAACAGTCCGCTGGAAACGCAACAAAAGGTCATCAACTGGGAGAAA 	TTCGCCGCAGGCCGAGTTATCCCGCGAGGCTACGGACTTGATAAGGAG 	GCTGACAAGC	rcactitgcggacatgcggaagcagaagcgccctacata
GAGAAGGAGAT!            GAGAAGGAGAT!	CTGAACCAAAAGG? 	TTCGTCAAACT               TTCGTCAAACT	ATCGATACCTC 	CGGAATCAGGT            CGGAATCAGGT	TGGGTGGTGAA             TGGGTGGTGAA	TACATACCAGGTC	CTGGCCAGATT( 	TCATTCACAG	CACCGACT	GAGAACGGCAA'                GAGAACGGCAA'	GGACCGAAGCC	rcgcrgg         rcgcrgg	SCAGCTGT 	GCCCTTT 	CTGCAT	TCTGTGC	TTCTTCAAG
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11;

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17; Indels

Mismatches Pred. No. 22;

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Best Local Similarity 91.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Colniker, S.E., Addams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
Holt, R.A., Evans, C.A., Gocayne, J.D.; Amanatides, P.G., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A.,
Carlson, J.W., Conter, A. Champe, M., Davenport, L.B., Dietz, S.M.,
Dodson, K., Dorsett, V., Doup, L.E., Doyle, C.; Dresnek, D., Farfan, D.,
Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A.,
Gonzalez, M., Houck, J., Hoskins, R.A., Höstin, D., Howland, T.J.,
Ibeywam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A.,
McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A.,
Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B.,
Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F.,
Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,
Zaveri, J.S., Smith, H.O., Rubin, G.M., and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (14-JUN-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
On or Defore Feb 24, 2001 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email
                                                                                                                                                        24-FEB-2001
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                                                                                                                                                   AC007821 163741 bp DNA linear INV 24-FEB-2001
Drosophila melanogaster, chromosome 3R, region 99F-100A, BAC clone
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2 (bases 1 to 163741)

Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.
Celniker,S.E., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
Butenhoff,C., Champe,M., Chavez,C., Chew,M., Clesiolka,L.,
Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
Noskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,
Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ţ
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
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5313 GAGGAAAACGCGGAGGAAATTCAACACTTATTCTCTGATAGCAACCGG 5360
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Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
This sequence was assembled using end sequences
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/strain="y: cn bw sp"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                   Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 163741)
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                                                                                                                                                                                                      complete sequence.
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DB 3;

Score 3969;

Query Match

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Db 107198 CAGAATTACACACCTCTGCGATACACGGCGACCAACGGACGCAACGATGCACTTACTCCT 107139
                                                                                                   Db 107138 GACTATCACCACGCCAAGCAGCCGATGGAGCACCCACCCTCCGCCTCCTCCTCCTGCTCCGGAC 107079
                                                                                                                                                                                                                                      107078 GIGGTCATACCGCCGCCGCCCGCCATTGTAGTAGGTCAGCCCGGAGCCGGCTCATATCCGTA 107019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106718 CGCAATCCCACCGCCTGCAGGCGGGCACGCCCCACCGCCGATGCCGCCCACTAGCCAG 106659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACTACCTGCGCTGCAGTCCGGCTCTGGACTCCGGAGCCGGTAGCTCCCGATCGGACAGC 1582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1583 CCCCATTCGCACCACACCACCACCACCGAGCTCGAGGACGGTGGGTAATCCAGGTGGAAAT 1642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1763 GCGTACGTGAAGCGGCGATCACCGGCCCTGAACAACGACCGCCGCCGGCGATAGCGCCACCC 1822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1823 ACTCAGCGMGGCAACTCACCTGTAATAACCCARAACGGGCTGAAGAACCCGCAGCAGCAG 1882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1883 TTGACGCAGCAGCTGAAGTCCCTGAACCTATACCCAGGCGGAGGCAGTGGAGCAGTKGTG 1942
                                                                                                                                                                                                                                                                                                                                                                          107018 TCCGGTGTGGGCGTTGGAGTGGTGGGTGTGCGAACGCACGTGTGCCAAAGATGATGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106598 ACTCAGCGGGCAACTCACCTGTAATAACCCAGAACGGCTGAAGAACCCGCAGCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCCTAATGCCAAACAGATCCGGAAGCCGAGCATCGAACGGGACACGGCGAGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106898 CACTACCTGCGCTGCAGTCCGGCTCTGGACTCCGGAGCCGGTAGCTCCGGATCGGACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1943, GAGCCACCGCCGCCCTACCTAATTCAAGGCGGAGCCGGAGCAGCAGCACCGCCGCCGCCA
                                                                                                                                                                                                                                                                                                                                       TCCGGTGTGGGGCGTTGGAGTGGTGTGGCGAACGGACGTGTSCCAAAGATGATGACG
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                                                                 1283.GACTATCACCACGCCAAGCCGATGGAGCCGCCACCCTCCGCCTCTCCTGCTCCGGAC
                                                                                                                                                                                                    1343 GTGGTCATACCGCCGCCGCCGCCATTGTAGGTCAGCCCGGAGCCGGCTCCATATCCGTA
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GTGCTGCAAACAGCAGTGGCGCCCCAATCGCCATCGAGTGCCTCGGCCAGCAATTCACCA	GTCCACGTGCTGGCCGCTCCACCTTTACCCTCAGAAGTCCGCGGCAGTGGTGCAGCGGGGGGGG	CAGCAACAGGCAGCGGCGGCCCACCAGCAGCAGCATCAGCACCAGCAACCAGCAACCAGCAACAGCAACCAGCAACCAGCAG	CCAACGCCMACCACCGCCCTTGGTGGTCTGAAYAGCAAGCCCAATTGCCTGGAGCCA	CCGTCCTATGCCAAGAGCATGCAGGCCAAGGCGGCACGGTGGTARAGCAGCAA	CAGCAGCAGCARCARCAGCAGGTCCAGCAGCAGCAGCAGCAACAGCAGCAGCAGCAGCAGCAG	CAACAGCAACTGCAGGCCTTGAGGGTGCTCCAGGCACAGGCTCAGA	-GGGAGCGGGATCAACGGGAGCGGGAACGGGATCAGCAGAAGCTGGCCAACGGAAATCCT 	GGCCGGCAGATGCTTCCGCCGCCGCCTATCAGAGCAACAACAACAACAACAACGAGGTC 	AAACCGCCGAGCTGCAACAACAACATACAGTAAGCAACACAGCAACCTGCGACGACACA	CCACCCATTCCGCCTGCCAAATAČAATAACAACTCCTCCAACACGGGGGGGGAATÁĆTCG 	GCCGCCACCAACGGATCCACCGCCACCACCTCCTCGTCGACGCTGCAAGATC	AAGCACGCCTCGCCCATCCCGGAGCGCAAGAAGATCTCCAAGGAGAGGAGGAGGGCCTTTTTTTT	AAGGAGTTCCGCATCAGGCAGTACTCGCCGCAAGCCTTCAAGTTCTTCATGAGCAGCACCTTCATTCTTCATGAGCAGCAGCACCTTCAAGTTCTTCATGAGCAGCAGCCAAGACCTTCAAGTTCTTCATGAGCAGCACACACA	ATAGAGAACGTGATCAAGTCGTATCGCCAGCGCAGGTATCGCAAGAATTCGCTGGAGAAG	GAGATGCACAAAGTGGGACTGCCCGATCAGACCCAAATCGAGATGAGGAAAATGCTGAAC 	CAAAAGAGAGAACTACATTCGATTGAACCGCCCAAGATGGACAAGAGCATGTTCGTC 	AAACTGAAGCCCATTGGAGTGGGTGCATTTGGCGAGGTAACGCTGGTGAGCAAAATCGAT	ACCTCGAACCATTGTATGCGATGAAAACCCTGCGGAAAGGGGACGTTCTCAAGCGGAAT 
106178	2303 106118	2363 106058	2423 105998	2483 105938	2540 105878	2600 105818	2646 105758	2705 105698	2765 105638	2825 105578	2885 105518	2945 105458	3005 105398	3065 105338	3125 105278	3185 105218	3245 105158	3305 105098
엄	Oy Dp	Qy Dp	Qy	Oy Db	Qy Db	Qy Dp	Qy Db	Oy Dp	Qy	Qy Dp	Oy Dp	9 P	Qy Pp	Qy Db	Qy Db	Oy Db	Oy Db	Oy Dp

	Qy	3365	CAGGTGGCACACGTGAAGGCCGAGAGGATATCCTCGCGGAAGCCGACAATAACTGGGTG 	3424 104979
	Qy Db	3425	GTGAAGTTGTACTACAGCTTCCAGGACAAGGATAATCTGTACTTTGTGATGGACTACATA	3484 104919
	ΟŊ	. 3485		3485
·,	QQ	104918	   CCAGGTGAGTGGAAACTTAAGCAGTCCAACGATGTGTATCGGAGTGCAAATGTCATTGTG	104859
•	QY	348	CAGGTGGTGATCTGATGTCGCTGCTCATCAAACTGGGCATTTTCGAGGAGGGGGGGTTTGTCGAGGAGGGGGGGG	3536 104799
	Οy	m	AACTGGCCAGATTCTACATCGCCGAGGTCACCTGCGCCGTGGACAGCGTTCACAAAATGG	969
	qq	10479	GCCCAGATTCTACATCGCCGAGGTCACCTGCGCCGTGGACAGCGTTCACAAAAT	104739
,	Oy Db	3597	GCTTCATT	3604
	3 8	340	A CASA CASA CASA CASA CASA CASA CASA CA	653
	qq	10467	TGGATTCATCCACAGAGACATCAAGCCTGACAACATACTCATCGATAGGGA	04
	Qy	3654	AAAGCTCACCGACTTTGGCCTGTGCACGGGATTCCGATGGACGCACAACTCGAAGTAC	3713
	qq	104618	TAAAGCTCACCGACTTTGGCCTGTGCACGGGATTCCGATGGACGCACAACTCGAAGTACT	104559
	QΫ	3714	CCAC	3724
,	Dp	104558	CAGGAGAACGGTO	104499
	Qy	3725	GCCAATCACTCGCGCAGGACTCGATGGAGCCCTGGGAGGAATA	3768
	qq	104498		104439
	Qγ	3769	ව <b>-</b>	3802
	Db	104438	CICCGAGAACGGACCGAACCCCACCGTGCTGAGAGGTGAGTTTCGTACACTTAATTAA	1.04379
	Óγ	3803	AGGCGATGCGCGATCACCAAA	3827
	QQ	104378	GGATCGGCCGTTAATAAAAGTATGCCGAACTCGCAGGCGACGGATGCGCGA	1-1
	QY	3828	GAGTCCTGGCCCACTCGCTGGTGGGCACCCCGAACTACATAGCTCCCGAGGTGCTGGAGA	3887
	ΩΩ	104318	CTGGCCCACTCGCTGGTGGCACCCCGAACTACATAGCTCCCGAGGT	104259
	ΟY	3888	GRAGTGGGTACACGCACTGTGCGACTACTGGAGCGTGGGCGTCATCCTYTAYGAGATGC	3947
Ť	QQ	104258	STGGGTACACGCAGCTGTGCGACTACTGGAGCGTGGGGCGTCATCCTCTATGAGAT	104199
	Qγ	3948	GGTGGGTCAGCCĠCCCTTTCTGG	3998
	qq	104198	STGGGTCAGCCCCTTTCTGGCCAACAGTCCGC	104139
	Qγ	3999		4004
	ΩD	104138	TAAAGCCAAGTGCATTACAACAATGACTTGCTTCATTTACAGGTC	104079
	Qy	4005	TCAACTGGGAGAAAACSCTGCATATTCCGCCGCAGGTGATCCCGCGGGGGTACGG	4064
	Dp	104078	TIGGGAGAAACCCTGCATATTCCGCCGCAGGCCGAGTTATCC	10
	Qγ	406	ACTTGATAAGGAGGCTCTGTGGGTCGGCTGACAAGCGGCTGGGCAAGAGCGTGGACGAGG	124
	qq	104018	- 🗀	103959

0 <u>y</u>	4125 103958	TCAACAGCCACGACTTCTTCAAGGGCATCGACTTTGCGGACATGCGGAAGCAGAAGGGC 418 	84 , 3899
O.Y	4185	AFCAAGCACCCRAGGGACACATCCAACTTTGATCCCGTGGATCCGG 42.	<b>4</b> 4
DB	103898		3839
OY	4245	GCTCGAATGACTCCACCATGAGCAGCGGCGATGATGTCGACCAGAATGACC 43	04
Db	103838		3779
QY	4305	GCACYTTCCACGCCTTTTTCCAATTTACCTTCCGTCGCTTTTTCGACGACAAGCAGCCGC 436	64
Db	103778		3719
Oy	4365	CGGATATGACGACGACGATCAGCGCTGTACGTCTGAAATGGATGCTCTCCATGTGCCC 442	24
Dp	103718		3659
Oy	4425	AGTCAAATAGTCACAAAAAGGGGATAGAA 44	84
Db			3599
Qy	4485	TGTAAAGGAAGCGTGGCTATAGAATGAAACTATCTATATA 45	<b>44</b>
Db	103598		3539
Qy	4545	CATTATATÀAATTATAGGACACAGTAGAGGCGGGACTACGTATATACATAC	04
Db	103538		3479
Oy	4605	GCCGTAGGCATGAACTGAATAAATAA 46	64
Dp	103478		3419
o	4665	CAGGACCTTCGACCTTTAACTG 47	24
o			3359
oy	4725	10	84
Dp	103358		3299
Oy	4785	AATTCAAAGGERCCAACTGGAAATCGAACCTTTCTGGTGCTCAAAGCAAGGCAAAGGAA 484	44
Db			3249
O.y Db	4845	10	04 · 3189
Oy Db	4905	CATCCGC 49	64 3129
Oy Dp	4965	CCATTCAGAATTGAGATTGCGAGGTGTGCGATGGAGAACGG 50	24 3069
Oy	5025	TATAAGCCTAATCTAAATCTAAA 50	3009
Dp	103068		
oy	5085	GTATGTCCTGCTATCCAATTCGTCTATCAC 51.	33
Dp			2949
oy Ob	5134 102948	ACGACCCCACCCCCCCCTCCCCATCCAAAAGAACAAAC 51.	89.
ΟŸ	5190	TIAGACGIAGCCIATGIGAAAAGCIAGCAATGIIAGACCAACTIGITGAATGCCAAATGA 524	. 64

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Drosophila melanogaster.

ENKaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;

ENKaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;

Bolkaryota; Belazoa, Enthropoda; Brachycera; Muscomorpha;

Rooptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

Stananatides, P. G. Scherer, S.E., Li, P. W., Hoskins, R.A.; Galle, R.F.,

Adams, M.D., Celniker, S.E., Holt, R.A.; Evans, C.A.; Gacayne, J.D.,

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George, R.A., Lewis, S.E., Richards, S., Ashburner, M., Henderson, S.N.,

Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, Q., Chen, L.X.;

Brandon, R.C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor

Miklos, G.L., Abril, J.F., Agbayani, A., An, H.J.,

Andrews Pfannkoch, C., Baldwin, D., Ballew, R.M., Basu, A.,

Baxendale, J., Bayraktaroglu, L., Beasley, E.M., Basu, A.,

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Baxendale, J., Burler, H., Cadieu, E., Center, A., Chandra, I.,

Cherry, J. M., Cavley, S., Dahlke, C., Davenport, L. B., Davices, P., de

Pablos, B., Delcher, A., Deng, Z., Mays, A.D., Dew, I., Dietz, S.M.,

Dodson, K., Doup, L.E., Downes, M., Dugan-Rocha, S., Dunkov, B.C.,

Chan, P., Harris, M., Harris, N.L., Harvey, D., Heiman, T. J.,

Hernandez, J. R., Houck, J., Hostin, M., Kalush, F., Karpen, G.H., Ke, Z.,

Kennison, J.A., Ketchum, R.A., Kimmel, D.E., Kodira, C.D., Kraft, C.,

Kravitz, S., Kulp, D., Lai, Z., Lasko, P., Lei, Y., Levitsky, A.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AE003775 236109 bp DNA linear INV 05-OCT-2000 Drosophila melanogaster genomic scaffold 142000013386035 section 100 of 105. complete sequence. AE003775 AE003775 GENERAL GI:7301969
Db 102888 TTAGACGTAGCCTATGTGAAAAGCTAGCAATGTTAGACCAACTTGTTGATGACCAAATGA 102829
                                                                                                                                   Db 102828 AATTGTTTAGCCCCACGAGGAAAACGCGGGGGAAATTCAACACTTATTCTCTGATAGCAA 102769
                                                                                                                                                                                                                 Db 102713 AATGTAATATTGTAAAGAACACGTTAATTGTAATCTATGCTAGAGTTGTGTAGCCCTA 102654
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                                                                                                                                                                                                                                                                                                                                                                                                                                      D 102653 AGATGTTTTTAGTTTATAGACCCCTAACCCTAATCTAGTTTAATTCCTAACACTAAGCG
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LOCUS
DEFINITION
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Li,J., Li,Z., Liang,Y., Lin,X., Liu,X., Mattei,B., McIntosh,T.C., McCledd,M.P., McPherson,D., Merkulov,G., Milshina,N.V., Modarry,C., Morris,J., Moshrefi,A., Mount,S.M., Moy,M., Murphy,B., Murphy,L., Muzny,D.M., Nelson,D.L., Nelson,D.R., Nelson,R.A., Nixon,K., Nixon,K., Sunskern,D.R., Parleb,J.M., Palazzolo,M., Pittman,G.S., Pan,S., Sollard,J., Puri,V., Reese,M.G., Reinert,R., Remington,K., Saunders,R.D., Scheeler,F., Shen,H., Spier,E., Spradling,A.C., Siapleton,M., Stupski,M.P., Smith,T., Spier,E., Spradling,A.C., Stapleton,M., Strong,R., Sun,E., Svirskas,R., Tector,C., Turner,R., Weinstock,G.M., Weissenbach,J., Williams,S.M., Woodage,T., Worley,K.C., Wu,D., Yang,S., Yao,Q.A., Ye,J., Yeh,R.F., Zaveril,J.S., Zhan,M., Zhang,G., Zhao,Q., Zheng,L., Zheng,R.P., Zhong,F.N., Zhong,W., Zhou,X., Zhu,X., Smith,H.O., The genome sequence of Drosophila melanogaster.
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complement(join(<23504. .23717,23771. .24048,24117. .24282,
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DMAAEENPAEKQONKRSDQEESOIKNLEENETVQEEEKLAKIMAAPALTAGEPEKVRL
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SSANSLSAATMQARTPSVESTVLPVPEPEPELPGVERFEVNRPFAYFIVDCQEQFVLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="FLYBASE:FBan0012069"
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complement(join(23504. .23717, 23771. .24048,24117. .24282,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 236109)
Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J. Direct Submission
Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rockville, MD, USA
Location/Qualifiers
1. 236109
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="FLYBASE:FBgn0039795"
join(20032. .21133,21223. >22071)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="FLYBASE:FBgn0039795"
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gene="CG1342"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="CG1342 gene product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(<23504. .>24751)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAF57075.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'chromosome="3R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="CG1342"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
MEDLINE
PUBMED
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REFERENCE AUTHORS

PEATURES

gene

mRNA

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/db_xref="FLYBASE:FBan0012066"
/db_xref="FLYBASE:FBan0000274"

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DDYEIKATLGSGSFGKVQLVRERESGVYXASKQLSKDQIVKTKQVSHVMSEKNVLRSM
                                                                                                                                                                                                                                                                                LHHCSLLYRDLKPENIMMDKNGYLKVTDFGFAKKVETRTMTLCGTPEYLPPEIIOSKP
YGTSVDWWAFGVLVFEFVAGHSPFSAHNRDVMSMYNKICEADYKMPSYFSGALRHLVD
                                                                                                                                                                                                                                                                                                                                               HLLQVDLSKRFGNLINGNRDIKEHEWFKDVEWIPLLNQTVNAPYVPNISNPEDISNFD
                                                                                                                                                                                                                                                      TFPNTVNLIASYKDFDSLYLVL.PLIGGGELFTYHRKVRKFTEKQARFYAAQVFLALEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(24899. .25229,25297. .25574,25629. .25794,
25875. .26104,26162. .26338))
/gene="pka-C2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KMHLMYRDLKPENILLDQRGYIKITDFGFTKRVDGRTSTLCGTPEYLAPEIVQLRPYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KSVDWWAFGILVYEFVAGRSPFAIHNRDVILMYSKICICDYKMPSYFTSQLRSLVESL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOVDTSKRKLERRLQRREESSVVPGRRLVWHSQPGSHRPLPAHHFRRRRSVELREIRV
QGSVQVPNKPPSRIVCEFLNVNVSFEIVVFFSVCLISRGAIVIGFCKSSFRNTALLLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Nucleotide sequence of the Celera sequence differs
from the published sequence for this transcript."
db_xref="FLYBASE:FBan0012066"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFLIYLVDSTKCFDYLYLILPLVNGGELFSYHRRVRKFNEKHARFYAAQVALALEYMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MSQHTSQYVFNSKEDYNVILDNMSREFEERWNHQTQSPYTNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MANRSSQRDREFNRDNTYNNNRDNRDHNRDNRDNRENRSNFQNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGYGYVEFETLAQLKSALNCNGRIKLDNFSAPLRIDIADHRRQNPGAPSGVGGAPPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPIQSITSINYNRITRGGFNSRVAVGGNGNRYQGGAPRNFNDREDQQSIGSGGFQRNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYNFNRSMNNSVGGGGAGVGRGGHPORNFNGNGGGGFGVVNGGGNYTNFVQNRNRDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VGHERGGGVGRGGSTGAANGNNPYYORRNYRRDDSVGSHQFRRREPRSNSSNHQMSNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENNHPVHGASESASSGTGPSSSNOFAVRDDDDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Pka-C2 gene product; Nucleotide sequence of the Celera sequence differs from the published sequence for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /ITRAVLGNGSFGTVMLVREKSGKNYYAAKMMSKEDLVRLKOVAHVHNEKHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="FLYBASE:FBgn0039797"
join(55458. .56524,56585. .>57119)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="FLYBASE:FBan0001340"
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                                                                                                                           /db_xref="FLYBASE:FBan0012069"
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                                                                                                                                                                                                                                                                                                                                                                                                              complement(<24899. .>26338)
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                                                                                                                                                                                                                                                                                                                                                                                 KVSDKPRPKAKTMRHEEAFADF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /map-"100A3-100A4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="CG12066"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="Pka-C2"
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	QY         2063 GACTACAGGAAATCCCCGAGCAGTGGGATATACTCGGCCACCTCGGCGGGCTCGCCGAGC         2122	183   GCCAGGAGTCAGCAGATCATCATCCAGAGTGTGAAGAGCACGCAGGTCCAAAAGCCC	2303 GTCCACGTGCTGGCCGCTCTTACCCTCAGAAGTCGGGGCAGTGGTGCAGG 2362 122784 GTCCACGTGCTGGCCGCTCTTACCCTCAGAAGTCGGGGCAGTGGTGCAGG 2362 122784 GTCCACGTGCTGGCCGCTCTTACCCTCAGAAGTCCGCGGCAGTGGTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	2423 CCAPGCCHACCACCGCCCTTGGTGGGTCTGAAYAGCAAGCCAATTGCCTGGAGCCA   1   1   1   1   1   1   1   1   1		Oy         2600         CAACAGCAACTGCAGGCTTTGAGGGTGCTCCAGGCACAGGCTCAGA	2705 GGCCGGCAGATGCTTCCGCCGCCCTATCAGAGCAACAACAACAACAACAGGGAGTC 2764 111111111111111111111111111111111111	DECEMBER   DECEMBER	2945 AAGCACCTCGCCCATCCGAGCGCAAGAAGATCTCCAAGAAGAAGAAGAGGAGGGCGCCTCGCCACCACCACCAGCAGGAGGAGGAGGAGGAGGGCGCCTCGCCGAGCCAAGAAGAATCTCCAAGGAGAAGAAGAGGAGGGCGCGCCATCCCGGAGCCAAGAAGAAGAAGAAGAAGAAGAAGAGAGGAG
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3AC	AAG NAG	AAC NAC	917 	GAT      GAT	AAT 	3GTG     3GTG	SATA	į	rGT(	GAG(	ATG     ATG	ì	O	CAC	STAC		AAT!	SAAS 	!	AATTAA	CCA CCA	GGA	GGA
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CATG	CAG 	AAA         AAA	SAGO	SAGO SAGO	ICT 	CAA	GAT      GAT	i	AAA	TTA	SGT		ATT	TAG       TAG	CAA	1	GTTTAACAGCTTT	0 - 0		STAC	555	CG	7900
CTIC	TAAT 	AGG 111	SAAC	3GT(       3GT(	CGT	CGA	TGT		TGC	93660	CAG		CAC	CGA 111 CGA	GCA 	1	AAC	GAG GAG	į	LTC	GGA.	CIG:	- <u>5</u>
GTTC	SAAG	SATC	GGA(	GCT GCT	GGA 	AGC  - -	CTT		3GA(	ACTO	GGA   GGA		AGT	CAT	GAC		TI	SATC		AGT	GAC	TAG	TAG
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CII	GTA	AAT     AAT	CAA	GGT 	SGAA 	1000	ATC ATC	1 + 1	TGT	CAT	00-00		rtat	ACA7	1000 1000	. }	CGT	GGA	9	GAG	4	T AC	Z Z Z
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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	Qy	3185	AAAAGGAGAGCAACTACATTCGATTGAAGCGCGCCAAGATGGACAAGAGCATGTTCGTC 324
	qa	1752	69
	ΟY	3245	CTGAAGCCCATTGGAGTGGGTGCATTTGGCGAGGTAACGCTGGTGAGCAAAATCGAT 330
	QQ	1692	3AAGCCCATTGGAGTGGGTGCATTTGGCGAGGTAACGCTGGTGAGCAAAATCGAT 163
	ΟY	3305	CGATGAAAACCCTGCGGAAAGCGGACGTTCTCAAGCGGAAT 336
	QQ	1632	TTGGAACCATTTGTATGGGATGAAACCCTGGGGAAAGGGGACGTTCTCAAGGGGAAT 157
	δĎ	3365	342
	qa .	1572	51
	Oy	3425	348
	Op	1512	GTGAAGTTGTACTACAGCTTCCAGGACAAGGATAATCTGTACTTTGTGATGGATACATA 1453
	Oy	3485	
	QΩ	1452	GGTGAGTGGAAACTTAAGCAGTCCAACGATGTGTATCGGAGTGCAAATGTCATTGTG 139
	ÓΫ	3486	GTGATCTGATGTCGCTGCTCATCAAACTGGGCATTTTCGAGGAGG 353
	QQ	1392	, 6
	ΟŊ	3537	SCCAGATTCTACATCGCCGAGGTCACCTGCGCCGTGGACAGCGTTCACAAAATGG
	qq	1332	27.
	δŏ	3597 (	CTTCATT360
	do	1272 (	21
	Qy	3605	365
	Op	1212	15
	QΣ	3654	AAAGCTCACCGACTTTGGCCTGTGCACGGGATTCCGATGGACGCACACTCGAAGTACT 371
	QΩ	1152	AAGTACT 109
	0y	3714 A	CCAGGAGAAC 372
	qq	1092 A	IIIIIIII CCAGGAGAACGGTGAGATGGAACCCCAGCTAACGTAGTTTAACAGCTTTAATATAT 103
	Óλ	3725 -	GGAGCCCTGC
	qq	1032 C	
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	qq	972 C	TCCGAGAACGGACCGAAGCCCACC
	Qγ	3803 -	
	qa .	13	AGGATCGGCCGTTAATAAAAGTATGCCGAACTCGCAGGCGGACGGA
•	δλ	3828 G	SGGCACCCGAACTACATAGCTCCCGAGGTGCT
	qq	852 G	-5
	οy	3888 GI	AAGTGGGTACACGCAGCTGTGCGACTACTGGAGCGTGGGCGTCATCCTYTAYGAGATGC 3947
	Dp	792 G	GAAGTGGGTACACGCAGCTGTGCGACTACTGGAGGGTGGGCGTCATCCTCTATGAGATGC 733

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For further information on this sequence
                                                     Location/Qualifiers
1. .39839
                                                                                                                          17.2%;
95.9%;
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Matches 1053; Conservative
          fly@celera.com.
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SEQUENCING IN PROGRESS ***, in ordered
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Drosophila melanogaster.

Burosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptear; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophilidae; Losophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 West Gude Drive,
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                 ACTTGATAAGGAGGCTCTGTGCGTCGGCTGACAAGCGGCTGGGCAAGAGCGTGGACGAGG
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                                                                                                                                                                                                                                                    Score 981.2; DB 2;
Pred. No. 1.7e-182;
5; Mismatches 9;
                              * NOTE: This is a 'working draft' sequence
* This sequence will be replaced
* by the finished sequence as soon as it
* the accession number will be preserved.
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/db_xref="taxon:7227"
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Pred. No. 3.3e-101;
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Nucleotide sequences of lats genes
Patent: US 6359193-A 7 19-MAR-2002;
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6359193.
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924 c, 894 g
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2929 CAGCTGCAAGAAGATCAAGCACGCCTCGCCCATCCCGGAGCGCAAGAAGATCTCCCAAGGA 2988
                                                                                                              CTTCATGGAGCAGCACATAGAGAACGTGATCAAGTCGTATCGCCAGCGCACGTATCGCAA 3108
                                                                                                                                                                                                        3529 CGAGGAGGAACTGGCCAGATTCTACATCGCCGAGGTCACCTGCGCCGTGGACAGCGTTCA 3588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3649 ACACATAAAGCTCACCGACTTTGGCCTGTGCACGGGATTCCGATGGACGCACAACTCGAA
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TSLDAKVLGSKDASRQQQMRATPKFGPYQKALREIRYSLLPFANESGTSAAAEVNRQM
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QAHQHPPKGYSTAVEPSAHFPGTHYGRGHLLSEQPGYGVQRSSSFQNKTPPDAYSSMA
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HVENVIKTYQQKVSRRLQLEQEVAKAGLCEAEQEGMRKILYQKESNYNRLKRAKMDKS
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EGAAEGCQPVYV"
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                                                                                                                                 AB023958 3460 bp mRNA linear ROD 09-MAR-2000
Mus musculus MmLATS2 mRNA for warts/lats-like kinase, complete cds.
                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                            Jenkins, N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (22-FEB-1999) Hiroshi Nojima, Research Institute for Microbial Diseases, Osaka University, Department of Molecular Genetics; Yamadaoka 3-1, Suita, Osaka 565-0871, Japan (E-mail:hnojima@biken.osaka-u.ac.jp, Tel:81-6-6875-3980,
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Y., Toji, S., Tanaka, H., Nishimune, Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                 homologue of the Drosophila tumor suppressor gene lats/warts Genomics 63 (2), 263-270 (2000)
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'db_xref="taxon:10090"
                                                                                                                                                                                                                      MmLATS2; warts/lats-like kinase.
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Sequence updated (06-Jan-2000).
Location/Qualifiers
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/gene="MmLATS2"
^no> c 963
                                                                                                                                                                                                                                                Mus musculus cDNA to mRNA.
                  2814 CCGCAGGTTCTTCGATGACAA 2834
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Nishiguchi, H., Endo, Y.,
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Nojima, H. and Fujii, T.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 5486)
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                                                                                              TGATCCCGTGGATCCGGAGAAGCTGCGCTCGAATGACTCCACCATGAGCAGCGGCGATGA 4287
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C12N15/09,A61K31/00,A61K38/27,C07K14/47,C07K14/525,C12Q1/68,
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CGAGGCTACGGACTTGATAAGGAGGCTCTGTGCGTCGGCTGACAAGCGGCTGGGCAAGAG
                                                3013 TGACCCGGTGGATGAAGAAAGCCCCTGGCACGAGGCCAGCGGAGAGAGCGCCCAAGGCCTG
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                                                                               CGTGGACGAGG----TCAAGAGCCACGACTTCTTCAAGGGCATCGACTTTGC---GGACAT
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1. 5486
Organism='Homo sapiens (human)'
Location/Qualifiers
1. 5486
/organism="Homo sapiens"
/db_xref="taxon:9606"
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4; Mismatches 493;
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Patent: JP 2000210086-A 1 02-AUG-2000;
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G12R1:91),C12N15/00,
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JP 2000210086-A/1
                                                                                                                                                                                                                                                                                       CCGCAGGTTCTTCGATGACAA 3153
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Best Local Similarity 64.1%;
Matches 964; Conservative
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2944 CAAGCACGCCTCGCCCATCCCGGAGCGCAAGAAGATCTCCAAGGAGAAGAAGGAGGAGGAGCA
                                        2102 GATTCAGACCTCTCCCGTTCCCGTCGCAAAACAGC-----AGAGACGAAGAAA
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              CCAGAATGACCGCACYTTCCACGGCTTTTTCGAATTTACCTTCCGTCGCTTCTTCGACGA
 GGAGAAACSCTGCATATTCCGCCGCAGGCCGAGTTATCCCGCGAGGCTACGGACTTGAT
                                                                                           4072 AAGGAGGCTCTGTGCGTCGGCTGACAAGCGGCTGGGCAAGAGCGTGGACGAGG---TCAA
                                                                                 GAGCCACGACTTCTTCAAGGGCATCGACTTTGC---GGACATGCGGAAGCAGAAGCGCC
                                                                                                                        CTACATACCGGAAATCAAGCACCCRACGGACACATCCAACTTTGATCCCGTGGATCCGGA
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1. 5486
Cocganism='Homo.sapiens (human)'
1. 5486
                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; E
Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                            DNA
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Koga,J., Kono,K. and N.Z.F.
Human tumor regulatory gene
Patent: JP 2000210086-A 2 02-AUG-2000;
NIHON CHEMICAL RESEARCH K K
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FT Source / Organism='Home
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/db_xref="taxon:9606"
1451 c 1388 g 1267
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25-JAN-1999 JP 1999016223
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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gene.
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JP 2000210086-A/2
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2042 GGGCGCCGACAAGAGCCCGCAAAAGCGCCAAGGGGGACAAAGGCCGGAAAGGATAAAAAGCA 2101
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                                                                                                                         CAAGGAGTTCCGCATCAGGCAGTACTCGCCGCAAGCCTTCAAGTTCTTCATGGAGCAGCA
                                                                                                                                              CATAGAGAACGTGATCAAGTCGTATCGCCAGCGCACGTATCGCAAGAATCAGCTGGAGAA
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PFANESGTSAAAEVNROMLQELVNAGCDQEMAGRALKQTGSRSIEAALEYISKMOYLD
PRNEQIVRVIKQTSPGKGLMPTPVTRRPSFEGTGDSFASYHQLSGTPYEGPSFGADGP
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Māmmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                  CTACATACCGGAAATCAAGCACCCRACGGACACATCCAACTTTGATCCCGTGGATCCGGA 4245
                                                                                                                                                                                                                                                                                  GAAGCTGCGCTCGAATGACTCCACCATGAGCAGCGGCGATGATGTC-----GA 4293
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                                                                                                                                                                                                                                                                                                                                                                       AB028019 3412 bp mRNA linear PRI 09-MAR-
Homo sapiens HsLATS2 mRNA for large tumor suppressor 2, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yabuta, N., Fujii, T., Copeland, N.G., Gilbert, D.J., Jenkins, N.A.
Nishiguchi, H., Endo, Y., Toji, S., Tanaka, H., Nishimune, Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (27-MAY-1999) Hiroshi Nojima, Research Institute for Microbial Diseases, Osaka University, Department of Molecular Genetics; Yamadaoka 3-1, Suita, Osaka 565-0871, Japan (E-mail:hnojima@biken.osaka-u.ac.jp, Tel:81-6-6875-3980,
                                                                                              CACCAAGCTGTGCTCCGCAGACCACCGCCTGGGGCGGATGGGGCCGATGACCTGAA
                                                                                                                                                                                                                                    GAGCCACGACTTCTTCAAGGGCATCGACTTTGC----GGACATGCGGAAGCAGAAAGCGCC
GGAGAAAACSCTGCATATTCCGCCGCAGGCCGAGTTATCCCGCGAGGCTACGGACTTGAT
                                                                    AAGGAGCTCTGTGCGTCGGCTGACAAGCGGCTGGGCAAGAGCGTGGACGAGG---TCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="large tumor suppressor 2"
/protein_id="BAA92381.1"
/db_xref="G1:7212790"
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Homo sapiens
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AVSAAHILHPVKSVRVLRPEPQTAVGPSHPAWVPAPAPAPAPAPAPAAAEGLDAKEEHA
                                                           LALGGAGAFPLDVEYGGPDRSÅRLRPTRSTCCCAKSEQYDLDSLCAGMEGSLRAGPNE
PEGGDKSRKSAKGDKGGKDKKQIQTSPVPVRKNSRDEEKRESRIKSYSPYAFKFFMEQ
                                                                                                                          MFVKIKTLGIGAFGEVCLACKVDTHALYAMKTLRKKDVLNRNQVAHVKAERDILAEAD
HKQAGPVAHQLHVLGSRSQVFASDSPPQSLLTPSRNSLNVDLYELSSTSVQQWPAATL
                                                                                                    HVENVIKTYQQKVNRRLQLEQEMAKAGLCEAEQEQMRKILYQKESNYNRLKRAKMDKS
                                                                                                                                              NEWVVKLYYSFQDKDSLYFVMDYIPGGDMMSLLIRMEVFPEHLARFYIAELTLAIESV
                                                                                                                                                                    HKMGFIHRDIKPDNILIDLDGHIKLTDFGLCTGFRWTHNSKYYQKGSHVRQDSMËPSD
                                                                                                                                                                                          LWDDVSNCRCGDRLKTLEQRARKQHQRSLAHSLVGTPNYIAPEVLLRKGYTQLCDWWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3304 TACCTCGAACCATTTGTATGCGATGAAAACCCTGCGGAAAGCGGACGTTCTCAAGCGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                                                                                                                                                                     Length 3412;
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4.4e-99;
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                                                                                                                                                                                                                                                                                                                                                                                                     Score 557;
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3364. .3369
/gene="HsLAIS2"
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                                                                                                                                                                                                                                                                                                                                                                                                                     64.18;
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HVAFREDCEVPSRTNSFNSHQPREGEPGKAEESLPANTAVTAAVTAAHILHPVKSVRVL
REPEQTAVGEBHAWVPARAPARAEPAPAAGELDAKEBHAALGGGAFELDVBKGE
PDRRCPPPYPKHLILKSKSEQTDLDSLCAGNEQSLARGPNEBEGGDKSRKSAKGDKG
GKÇKKQIQTSPVPVRKNSRDEEKRESRIKSYSPIAFKFFMEQHVENVIKTYQQKVNRR
                                                                                                                                                                                                                                                                                                                  /trānslation="MRPKTFPATTYSGNSRQRLQBIREGLKQPSKSSVQGLPAGPNSD
TSLDAKVLGSKDATRQQQQMRATPKFGPYQKALREIRYSLLPFANESGTSAAAEVNRQ
MLOELVNAGCDQEMAGRALKQTGSRSIEAALEYISKMGYLDPRNEQIVRVIKQTSPGK
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SQVFASDSPPQSLLTPSRNSLNVDLYELSSTSVQQWPAATLARRDSLQKPGLEAPPRA
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CLACKVDTHALYAMKTLRKKDVLNRNQVVHVKAERDILLAEADNEWVVKLYYSFQDKDS
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APTPTETQLKVINWENTLHIPAQVKLSPEARDLITKLCCSADHRLGRNGADDLKAHPF
FSAIDFSSDIRKQPAPYVPTISHPMDTSNFDPVDEESPWNDASEGSTKAWDTLTSPNN
                                                                                                                                                                                                                                                                                                                                                                     GLMPTPVTRRPSFEGTGDSFASYHQLSGTPYEGPSFGADGPTALEEMPRPYVDYLFPG
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                                                                                   Oncology, Kyoto University,
Kyoto Prefecture 606-8507,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2030 GGGCGGCGACAAGAGCCGCAAAAGCGCCCAAGGGGGAAAGGCGGAAAGGATAAAAAGCA 2089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  494; Indels
                                                                                                                                                                                                                  375. .3641
/note="similar to Drosophila warts/lats"
                                                                                                                                                                                                                                                                /product-"serine/threonine kinase KPM"
/protein_id="AAF80561.1"
/db_xref="GI:8886764".
                                                                                                                                                                                                    /tissue_type="myeloid cell line"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   '; DB 9;
4.5e-99;
                                                        Direct Submission
Submitted (20-NOV-1999) Hematology and
54 Kwaracho, Shogoin, Sakyoku, Kyoto,
Japan
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Pred. No. 4
                                                                                                                                                                                   /db_xref="taxon:9606
                                                                                                                                   Location/Qualifiers
                                                                                                                                                                    /organism="Homo
                                                                                                                                                                                                                                                    /codon_start=1
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                              2 (bases 1 to 4098)
Hori, T.
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CACCAAGCTGTGCTCCGCAGACCACCGCCTGGGGCGGAATGGGGCCGATGAA
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                                                                                                                                                    GAGCCATGTCAGACAGGACAGCATGTCTGGGATGATGTCTAGTGTCTGTAGTGT
                                                                                                                                                                                                 ---GAACGGACCGAAGCCCACCGTGCAGAGGCGACGGATGCGCGATCACCAAAGAGT
                                                                                                                                                                                                                              TCGGTGTGGGGACAGGCTGAAGACCCTAGAGCAGAGGGGCGCGGGAAGCAGCACCAGAGGTC
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                                                                CGACTITGGCCTGTGCACGGGATTCCGATGGACGCACAACTCGAAGTACTACCAGGAGA-
                                                                                                                                                                                                                                                                                                                               TGGGTACACGCAGCTGTGCGACTACTGGAGCGTGGGCGTCATCCTYTAYGAGATGCTGGT
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kinase KPM mRNA, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Homo sapiens serine/threonine
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VERSION
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AUTHORS
TITLE
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Qy 435 Db 351	RESULT 1 AR201456 LOCUS	DEFINITI ACCESSIO VERSION	SOURCE ORGANI	REFERENC	TITLE JOURNA	SOU.	ORIGIN	Query Dest Lo	Oy 2984	Db 1354	Oy 3044	Db 1414	Oy 31,04 Db 1474	Qy 3164	Db 1534	Qy 3224	Db 1594			Oy 3344		Db 1771	Oy 3464	Db 1831	Qy 3524	Db 1891	y 3584	b 1951
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3304 TACCTCGAACCATTGGGATGAAAACCCTGGGAAAGCGGACGTTCTCAAGGGGAA 3363 	3364 TC. 11 2498 TC.	3424 GGTGAAGTTGTACTACAGCTTCCAGGACAAGGATAATCTGTACTTTGTGATGGACTACAT 3483 	3484 ACCAGGTGGTGATCTGATGTCGCTGCTCAAACTGGGCATTTTCGAGGAGGAACTGGC	2618			CGACTTTGCCCTCTCTACCTATTTTTTTTCTCCCATTTTTTTCTCCCCCC	2798 AGATTTCGGCCTCTCCACTGGGTTCAGGACACTCCAAATTCCAAATACTGGGAA- 3722		g		CCTGGCCCATTCGTTCGTTCGCATCCTAGATCATAGATCAGGCGCGGAAGCAGCAGGTG 2		3892 TGGGTACACGCACTGTGCGACTACTGGAGCGTGGGCGTCATCCTYTAYGAGATGCTGGT 3951				4012 GGAGAAAACSCTGCATATTCGGCGGAGGTTATCCGGGAGGCTAGGACTTGAT 4071 3158 GGAGAACAGGTCCAAATTCCAGTGAGAGAGTGAAAAAAAA		3218 CACCAAGCTGTGCTGCTGCAGCACCACCGCGTGGGAATGGGGCCGATGAGAGTGAA 3277	GAGCCACGACTTCTTCAAGGGCATCGACTTTGCGGACATGCGGAAGCAGAAAGGGCC						4294 CCAGAATGACCGCACYTTCCACGCTTTTTCGAATTTACCTTCCGTCGCTTCTTCGACGA 4353	3458 CAATAACAAGCATCTGAGCACGCATTTTACGAATTCACCTTCCGAAGGTTCTTTGATGA 3517
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         linear
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X.T., Tao,W., Wang,W., Zhang,S. and Yu,W.
Nucleotide sequences of lats genes
Patent: US 6359193-A 5 19-MAR 2002;
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Sequence 5 from patent US 6359193.
AR201456
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Murinae; Mus
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IdentifyIng tumor suppressors in genetic mosaics: the Drosophila
lats gene encodes a putative protein kinase
Development 121 (4), 1053-1063 (1995)
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Chen,W. and Xu,T.
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                                                                       118 GCTGCTCGCCAGCACCAGCGATGTCTAGCCCATTCTCTGGTTGGGACTCCCAATTATATT
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St John,M.A., Tao,W., Fei,X., Fukumoto,R., Carcangiu,M.L.
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Sciurognathi; Muridae;
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Mus musculus large tumor suppressor 1 (Lats1) mRNA,
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Mammalia; Eutheria; Rodentia;
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SLVGTPNYIAPEVLLRTGYTQLCDWWSVGVILCEMLVGQPPFLAQTPLETQMKVIIWQ
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SYIPKITHPTDTSNFDPVDPDKLMSDGSEEENISDTLSGWYKNGKHPEHAFYEFTFRR
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                           ovarian
                                                                                                                                                                          Tao,W. and Xu,T.
Direct Submission
Submitted (04-NOV-1998) Genetics, HHMI, Yale University, 295
Congress Ave BCMM 254D, New Haven, CT 06536, USA
Location/Qualifiers
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21 (2), 182-186 (1999)
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/db_xref="taxon:10090"
/tissue_type="brain"
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Parlow, A.F.,
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Fruit fly; Lats; large tumour suppressor; cytostatic; vulnerary; cell overproliferation inhibitor; edc2; cell cycle-dependent kinase; treatment; prevention; screening; cancer; skin; ovarian tumour; soft tissue sarcoma; pituitary disorder; gene therapy; hyperplasia; LH; lutelnising hormone hypogonadotropic hypogonadism; metaplasia; dysplasia; degenerative disorder; growth deficiency; physical trauma; hypoproliferative disorder; lesion; wound; lats knock-out mouse; ds.
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S; Zhang RK, Fukumoto Fei X, Stewart RA; John st Xu T, Tao W, Turenchalk GS, Xu T,

WPI; 2000-246496/21. P-PSDB; AAY70393. Use of lats proteins, complexes of lats and cdc2 for treating cancer that is refractory to treatment by standard chemotherapy and radiation therapy, and disorders associated with aberrant levels of cdc2 activity

Claim 44; Fig 15; 134pp; English

The present sequence is a DNA encoding Drosophila Lats (large tumour suppressor) protein which is a cell overproliferation inhibitor and a negative requiator of cell cycle-dependent kinase cdc2/cyclin A.

The present sequence is useful for treating cancer that is refractory to standard chemotherapy or radiation therapy such as hyperplasia.

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C to standard chemotherapy or radiation therapy such as hyperplasia.

C to standard chemotherapy or radiation therapy such as hyperplasia.

C to standard chemotherapy or radiation therapy such as hyperplasia.

C to standard degenerative disorders, growth deficiencies, hypoproliferative disorders, protein and sorders, preferably a mouse, in which a lats gene has been disrupted by homologous compounds that can be used to treat or prevent cancer, particularly skin cancer, soft tissue sarcomas and ovarian tumours, and disorders compound that the lats of the lats of the lats of the perapy. 

Sequence 5720 BP; 1684 A; 1491 C; 1457 G; 1088 T; 0 other;

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ò á	3721	GAACGCCAATCACTCGCGCCAGGACTCGATGGAGCCCTGGGAGGAATACTCCCGAGAACGG 37	Oy Db	4801 ACTGG
6y			- OA	4861
q	3781	1 ACCGAAGCCCACCGTGCAGAGGCGACGGATGCGCAAACAGTCACCAAAGAGTCTCTGGCCCA 3840	ପ୍ର ଓ	4861 TTAAA
ζ, g	3841	1 CTCGCTGGTGGGCACCCCGAACTACATAGCTCCCGAGGTGCTGGAGAGAGGGGTACAC 3900 	A A A A A A A A A A A A A A A A A A A	4921
δ d	3901.	GCAGCTGTGCGACTACTGGAGCGTGGCGTCATCCTTTAYGAGATGCTGGTGGGTCAGCC	do do	4981 CATTCA 
a ò	3961		00	5041
7 A	3961	GCCCTTTCTGGCCAACAGTCGCTGGAAACGCAACAAAAAGGTCATCAACTGGGGAAAAAC	qa :	5041
oy a	4021	SCTGCATATTCCGCCGCAGGCCGAGGTTATCCCGCGAGGTACGGACTTGATAAGGÄGGCT	do O	5101 YATGTA 
g ò	4021		QV	5161
G G	4081	CTGTGCGTCGGCTGACAAGCGGCTGGGCAAGAGCGTGGAGGCTCAAGAGCCACGTTTTTTTT	q <sub>Q</sub>	5161
ογ	4141	1 CTTCAAGGGCATCGACTTTGCGGACATGCGGAAAGGGGCCCTACATACCGGAAT 4200	9y 0d	5221 GTTAGP          5221 GTTAGP
<u>අ</u> ,	4141	CTTCAAGGGCATCGACTTTGCGGACATGCGGAAGCAGAAAAGCGCCCCTACATACCGGAAAT	, vo	. 5281
ò a	4201	1 CARGCACCCRACGRACACTOCAACTTTGATCCCGTGGATCCGGAGAAGCTGCGCTCGAA 4260	a a	
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Oy Dp	4321	TITGAATTIACCTICGGTGGCTTCTTGGACGAGGAGCGCCGCGGATATGACGGAGGA 4380 	δ d d	5401 AATCTA 
δλ	4381	TCAGGCGCCGGTTTACGTCTGAAATGGATGCTCTCCATGTGCCCAACACCCAACACCCCGC 4	QY	5461 TAATCT
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Qy	4561	GGGGGCAGTAGAGGCGGGGGGGTACGTATATACATACAAATATATAT	Οy	
qq	4561	GGAGACAGTAGAGGCGGGAGCTACGTATATACATACAAATAATATACATATATTTGATAT 4620	qq .	
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λo ά	4741	GTGCACTACTACTACACAAATATATATTTTAAATTGTTAGAATTCAAAAGGGGCCA 	X X X	AAT42117;
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This sequence encodes the Drosophila melanogaster large tumour suppressor lats protein, and is a composite of 2 cDNAs (an initial fragment from cDNA-9 and the rest from cDNA-A2). The sequence has been isolated from a total imaginal disc cDNA library. The corresponding genomic sequence is identical, except. for 34 minor differences, and has 7 introns. Two consensus polyadenylation sites are present. A 141-bp sequence at the 3'-end of the lats transcript is identical to the 5'-end of the untranslated sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                  · used to develop prods
                                                                                                                                                                                                                                                                                                                                                                                           New isolated large tumour suppressor gene - used to develop prode for inhibiting cell proliferation or for enhancing proliferation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence data for this patent did not form part of the printed cification, but was obtained in electronic format directly from
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developmental biology; cell signalling; insecticide;

polynucleotide

Drosophila melanogaster expressed

pharmaceutical; gene; ss Drosophila melanogaster.

Drosophila;

WO200171042-A2

27-SEP-2001

(first entry)

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detection reagent for detecting 1000 or mon for elucidating cell signalling and cell-ce

New isolated nucleic acid of genes from Drosophila and interactions

Ε¥ Myers

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/enter JC, Adams M, WPI; 2001-656860/75. P-PSDB; ABB59066.

(PEKE ) PE CORP NY.

23-MAR-2001; 2001WO-US09231 23-MAR-2000; 2000US-191637P 11-JUL-2000; 2000US-0614150 Claim 1; SEQ ID NO 3989; 21pp + Sequence Listing; English.

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and
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                                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical furgs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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ž q	1643	GGTGGATTITCTCCGTCGCCAAGCGGTITCAGTGAGGTGGCTCCACCGCCGCCGCCCCCA 1702 	
ž q	1703	CGCAATCCCACCGCCTSCAGCGCGGCCACGCCCCACGCCCAGGCCGCCCCACCAGCCAG 1762 	
Sy Ob	1763 661	GCGTACGTGAAGCGGCGATCACCGGCCCTGAACAACCGCCGGCGGCGATAGCGCCACCC 1822 	
δ qα	1823	ACTCAGCGMGGCAACTCACCTGTAATAACCCARAACGGGCTGAAGAACCCGCAGCAGCAG 1882 	
Qy Db	1883	TTGACGCAGCAGCTGAAGTCCCTGAACCTATACCCAGGCGGAGGCAGTGGAGCAGTKGTG 1942 	
. og op	1943	GAGCCACCGCCGTACCTAATTCAAGGCGGAGCGGAGGAGCAGCGCGCGC	
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S S	2183	GCCAGGAGTCAGCAGCCGATCATCATGCAGAGTGTGAAGAGCACGCAGGTCCAAAAGCCC 2242 	
Oy Op	2243	TCTGCGAACAGCAGTGGCGCGCCAATCGCCATT	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse; m-lats2 gene; large tumour suppressor; fetal brain; protein-sering-threonine-Kinase; cell proliferation; antisense; dominant-negative; cancer; degenerative disorder; trauma; growth deficiency; therapy; antitumour; vulnerary; diagnostic; transgenic plant; transgenic animal; growth; senescence; ds.
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                                                                            m-lats2 protein
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                                                          TGTGATGGACTACATACCAGGTGGTGATCTGATGTCGCTGCTCATCAAACTGGGCATTTT
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The present sequence is a DNA encoding mouse Lats2 (large tumour suppressor) protein which is a cell overproliferation inhibitor and a negative regulator of cell cycle-dependent kinase cdc2/cyclin A. The present sequence is useful for treating cancer that is refractory to standard chemotherapy or radiation therapy such as hyperplasia, metaplasia, or dysplasia, and disorders associated with aberrant levels of cdc2 activity. Conditions treated by promoting cdc2 function include degenerative disorders, growth deficiencies, hypoproliferative disorders, physical trauma, lesions, and wounds. An animal model preferably a mouse, in which a lats gene has been disrupted by homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of lats proteins, complexes of lats and cdc2 for treating cancer that is refractory to treatment by standard chemotherapy and radiation therapy, and disorders associated with aberrant levels of cdc2 activity
                                                                                                                                                                                                                                                                                                                                                                                                                                         cell overproliferation inhibitor; cdc2, cell cycle-dependent kinase; treatment; prevention; screening; cancer; skin; ovarian tumour; soft tissue sarcoma; pituitary disorder; gene therapy; hyperplasia; liH: luteinizing hormone hypogonadotropic hypogonadism; metaplasia; dysplasia; degenerative disorder; growth deficiency; physical trauma; hypoproliferative disorder; lesion; wound; lats knock-out mouse; ds.
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/note= "This region is erroneously repeated in the
mouse Lats2 DNA sequence shown in figure 14"
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DNA sequence shown in figure 14"
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recombination, e.g. a lats knock-out mouse, is used for screening compounds that can be used to treat or prevent cancer, particularly skin cancer, soft tissue sarcomas and ovarian thumours, and disorders associated with pituitary dysfunction e.g. luteinizing hormone (LH) hypogonadotropic hypogonadism. The lats DNA is also used in gene therapy.
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                                                                                 Score 567.8; DB 21; Length 3155;
Pred. No. 6.3e-110;
4; Mismatches 491; Indels 48;
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GGACGATGTTTCCAACTGTCGCTGTGGAGACAGGTTAAAGACCCTGGAGCAGAGGGCGCA
                                                                                                                                                                                                                    ACAAAAGGTCAŢCAACTGGGAGAAAACSCTGCATATTCCGCCGCAGGCCGAGTTATCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    signal transduction;
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This is the nucleotide sequence of a cDNA clone coding for a human crthologue, i.e. hWART2 (see AAY06527), of Drosophila non-receptor serine/threonine kinase WART.

Serine/threonine kinase WART.

CONSTRUCTION AND IDEATH OF THE STOCK WAS ISOLATED FOR A human bone marrow cDNA library using a PCR fragment of hWART1 as probe. hWART2 is consistently expressed in human tumour cells tines, exceptfor most of the colon cancer lines examined. This overexpression in tumour cells versus normal tissues may provide a target for oncology drug development. Nucleic acids encoding full-length hWART2 and hWART2 polypeptides lacking one or more of and anno acid segments 1-33, 43-139, 342-466, 467-480, 514-518, and 974-1048, or lacking one or more of the N-terminal domain, catalytic domain, or C-terminal domain are claimed, as well as antibodies, a method for identifying modulators of hWART function, and use of such modulator compounds to treat an abnormal condition involving hWART signal transduction, especially cancer. Probes for
                                                                                                                                                                                                                             treating cancer
                                                                                                                                                                                                   New nucleic acid encoding human orthologs of Drosophila WART proteins, used to identify specific modulators for treating (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               involving hWART signal transduction, especially or detection of hWART nucleic acids are also claimed
                                                                                                                                                                                                                                                                                            Claim 1; Page 122-123; 137pp; English
98US-0072023
                                                                                        g;
                                                                                      Flanagan P, Plowman
                                                                                                                                  WPI; 1999-458698/38
                                         (SUGE-) SUGEN INC
                                                                                                                                                                                                                                                    for diagnosis
                                                                                                                                                         P-PSDB; AAY06527
  21-JAN-1998;
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Sequence 5276 BP; 1348 A; 1407 C; 1345 G; 1176 T; 0.other;

2200 3243 2380 3303 3423 2884 GGGCGCCACCAACGGATCCACCGCCACCGCCTCCTCGTCGACCAGCAGAAGAT 2943 2141 GAGAGAGTCACGCATCAAGAGCTACTCGCCATACGCCTTTAAGTTCTTCATGGAGCAGCA CATAGAGAACGTGATCAAGTCGTATCGCCAGCGCACGTATCGCAAGAATCAGCTGGAGAA CGTGGAGAATGTCATCAAAACCTACCAGCAGAAGGTTAACCGGAGGCTGCAGCTGGAGCA TACCTCGAACCATTTGTATGCGATGAAAACCCTGCGGAAAGCGGACGTTCTCAAGCGGAA CAAGGAGTICCGCATCAGGCAGTACTCGCCGCAAGCCTTCAAGTTCTTCATGGAGCAGCA AGAAATGGCCAAAGCTGGACTCTGTGAAGCTGAGGAGGAGCAGATGCGGAAGATCCTCTA 3124 GGAGATGCACAAAGTGGGACTGCCCGATCAGACCCAAATCGAGATGAGGAAAATGCTGAA TCAGGTGGCACACGTGAAGGCCGAGAGGATATCCTCGCGGAAGCCGACAATAACTGGGT CCAAAAGGAGAACTACATTCGATTGAAGCGCGCCAAGATGGACAAGAGCATGTTCGT CAAACTGAAGCCCATTGGAGTGGTGCATTTGGCGAGGTAACGCTGGTGAGCAAAATCGA 9.8%; Score 558.6; DB 20; Length 5276; 64.1%; Pred. No. 6.9e-108; Indels 4; Mismatches 493; Conservative Similarity Best Local Sim Matches 964; Query Match 2944 2090 2201 2261 3064 3004 3184 3244 3304 2381 2441 3364 a á g ò ò a ò . ð 9 ð g ò 엄 ò g ò

RESULT 8

3663 3097 4245 3831 2977 3891 3037 4011 3157 4071 3277 3458 CAATAACAAGCATCCTGAGCACGCATTTTACGAATTCACCTTCCGAAGGTTCTTGATGA 3517 3338 CTACGTTCCCACCATCAGCCCCCATGGACACCTCGAATTTCGACCCCGTAGATGAAGA 3397 2918 TCGGTGTGGGGACAGGCTGAAGACCCTAGAGCAGAGGCGCGCGGAAGCAGCAGAGGG 2978 CCTGGCACATTCACTGGTGGGGACTCCAAACTACATCGCACCCGAGGTGCTCCTCGCAA 2498 TCAGGTGGCCCACGTCAAGGCCGAGAGGGACATCCTGGCCGAGGCAGACAATGAGTGGGT 2558 GGTCAAACTCTACTACTTCCAAGACAAAGACAGCCTGTACTTTGTGATGACTACAT ---GAACGGACCGAAGCCCACCGTGCTGGAGAGGCGACGGATGCGCGATCACCAAAGAGT CCTGGCCCACTCGCTGGTGGCACCCCGAACTACATAGCTCCCGAGGTGCTGGAGAGRAG GCTGAAGTTGTACTACAGCTTCCAGGACAAGGATAATCTGTACTTTGTGATGGACTACAT 2618 CCCTGGTGGGGACATGATGAGCCTGCTGATCCGGATGGAGGTCTTCCCTGAGCACCTGGC CAGATTCTACATCGCCGAGGTCACCTGCGCCGTGGACAGCGTTCACAAAATGGGCTTCAT 2738 CCACCGAGACATCAAGCCTGATAACATTTTGATAGATCTGGATGGTCACATTAAACTCAC CGACTTTGGCCTGTGCACGGGATTCCGATGGACGCACAACTCGAAGTACTACCAGGAGA-----ACGGCAATCACTCGCGCCAGGACTCGATGGAGCCCTGGGAGGAATACTCCGA---GAGCCATGTCAGACAGGACAGCATGTCTGGGATGATGTGTTCTAACTG GGGTCAGCCGCCCTTTCTGGCCCAACAGTCCGCTGGAAACGCAACAAAAGGTCATCAACTG 4012 GGAGAAAACSCTGCATATTCCGCCGCAGGCCGAGTTATCCCGCGAGGTTACGGACTTGAT 4072 AAGGAGGCTCTGTGCGTCGGCTGACAAGCGGCTGGGCAAGAGCGTGGACGAGG---TCAA GAGCCACGACTTCTTCAAGGCCATCGACTTTGC---GGACATGCGGAAGCAGAAAGCGCC 4186 CTACATACCGGAAATCAAGCACCCRACGGACACATCCCAACTTTGATCCCGTGGATCCGGA 3398 AAGCCCTTGGAACGATGCCAGCGAAGGTAGCACCAAGGCCTGGGACACACTCACCTCGCC CCAGAATGACCGCACYTTCCACGCCTTTTTCGAATTTACCTTCCGTCGCTTCTTCGACGA ACCAGGTGGTGATCTGATGTCGCTGCTCATCAAACTGGGCATTTTCGAGGAGGAACTGGC GGAGAACACGCTCCACATTCCAGCCCAGGTGAAGCTGAGCCCTGAGGCCAGGGACCTCAT GAAGCTGCGCTCGAATGACTCCACCATGAGCAGCGGCGATGATGTC 4354 CAA 4356 CAA 3520 3544 3664 2858 3832 3952 3158 4129 4246 3424 3484 3723 3775 3518 4294 ò g 9 ò a ŏ qq ŏ g g qq οp ò ò ò Db δ g δ q δ ò g δy g g òγ

3243 2392 3303 3363

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2213 CGTGGAGAATGTCATCAAAACCTACCAGCAGAAGGTTAACCGGAGGCTGCAGCTGGAGCA
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                                             CAAACTGAAGCCCATTGGAGTGGTTTTGGCGAGGTAACGCTGGTGAGCAAAATCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes a human growth hormone inhibited tumour suppressor (hGHITS) proteins. The hGHITS proteins can be used in an antineoplastic pharmaceutical preparation. Probes for the hGHITS DNA sequences can be used in diagnostic pharmaceutical preparations can be used for examining expression of hGHITS genes in dwarfism, gigantism, acromegaly, angiopathy, diabetic nephropathy or cardiopathy, or in malignant tumours including breast cancer, renal adenocarcinoma, colorectal cancer, and leukaemia. Antibodies against the proteins can be used is diagnostic pharmaceutical preparation for examining expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 tumour suppressor genes 1 and 2
acromegaly, angiopathy, diabetic
                                                                                                        tumour suppressor protein; hGHITS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 5486;
                                                                                                                   antineoplastic; dwarfism; gigantism; acromegaly; angiopathy; diabetic nephropathy; cardiopathy; tumour; breast cancer; renal adenocarcinoma; colorectal cancer; leukaemia; ss.
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Pred. No. 7e-108;
4; Mismatches 493;
                                                                             a tumour suppressor protein hGHITS1
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387..3653
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5486
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964; Conservative
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                                                     entry)
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 DNA;
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P-PSDB; AAB07633.
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 standard;
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AAA59129
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Best Local S
Matches 964
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3603 2749 3663 2809 3722 2869

3774

3831 2989 3891 3049

3951

3169

4011

4128

4071

Length 5486;

DB 21;

9.8%; Score 558.6; 64.1%; Pred No. 7e-

Similarity

Query Match Local

BP; 1380 A; 1451 C; 1388 G; 1267 T; 0 other;

Sequence 5486

. OS

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3409
                                                                        3469
                                                                                                       4353
                                                   4293
                                                                                                               New human growth hormone inhibited tumour suppressor genes 1 and 2 for diagnosis of dwarfism, gigantism, acromegaly, angiopathy, diabetic nephropathy or cardiopathy
CTACATACCGGAAATCAAGCACCCRACGGACACATCCAACTTTGATCCCGTGGATCCGGA
               3410 AAGCCCTTGGAACGATGCCAGCGAAGGTAGCACCAAGGCCTGGGACACACTCACCTCGCC
                                                     -----GA
                                                                                                  CCAGAATGACCGCACYTTCCACGCTTTTTCGAATTTACCTTCCGTCGCTTCTTCGACGA
                                                                                                                                                                                                                                                                                                                                         Human; growth hormone inhibited tumour suppressor protein; hGHITS; antineoplastic; dwarfism; gigantism; acromegaly; andiopathy; diabetic nephropathy; cardiopathy; tumour; breast cancer; renal adenocarcinoma; colorectal cancer; leukaemia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/product= "tumour suppressor protein"
                                                 GAAGCTGCGCTCGAATGACTCCACCATGAGCAGCGGCGATGATGTC-
                                                                                                                                                                                                                                                                                                                   encoding a tumour suppressor protein hGHITS2
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The present sequence encodes a human growth hormone inhibited tumour suppressor (hGHTS) protein. The hGHTS proteins can be used in an antineoplastic pharmaceutical preparation. Probes for the hGHTS bunk sequences can be used in diagnostic pharmaceutical preparations. The diagnostic pharmaceutical preparations can be used for examining expression of hGHTS genes in dwarfiam, gigantism, acromegaly, ampiopathy, diabetic nephropathy or cardiopathy, or in malignant tumours including breast cancer, renal adenocarcinoma, colorectal cancer, and lenkaemia. Antibodies against the proteins can be used in a diagnostic pharmaceutical preparation for examining expression of tumour suppressor gene.

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GGAGAACACGCTCCACATTCCAGCTCAGGTGAAGCTGAGCCCTGAGGCCAGGGACCTCAT 3229
                                                                                                                                                                                                                                                                          AAGCCCTTGGAACGATGCCAGCGAAGGTAGCACCAAGGCCTGGGACACACTCACCTCGCC 3469
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           TGGGTACACGCAGCTGTGCGACTACTGGAGCGTGGGCGTCATCCTYTAYGAGATGCTGGT
                                                                                 GGAGAAAACSCIGCATATICCGCCGCAGGCCGAGTIATCCCGCGAGGCTACGGACTIGAT
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                                                                                                                                                                                                                                                      GAAGCTGCGCTCGAATGACTCCACCATGAGCAGCGGCGATGATGTC----
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/note= "partial sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes a partial polypeptide which has kinase activity. The kinase polynucleotides can be used to express the polypeptides, and as probes to identify nucleic acids encoding proteins having kinase activity. The kinase polypeptides and fragmented polypeptides are used as molecular weight and isoelectric focusing markers, and as controls for peptide fragmentation. They als have a number of therapeutic uses as kinases play a central role in cellular signal transduction. The polypeptides could also be used a reagent to identify any proteins. The polypeptides can also be used a reagent to identify any proteins that the polypeptide regulates, an proteins with which it might interact. The polypeptides may also be used for preparation of antibodies. The antibodies can be used in assays to detect the presence of the protein, and to purify the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 GATTCAGACCTCTCCCGTTCCCGTCCGCAAAACAGC------AGAGACGAAGAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1961;
              New numan kinase polypeptides and polynucleotides used as
weight markers and as controls for peptide fragmentation
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1961 BP; 504 A; 550 C; 539 G; 368 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 9.7%; Score 557; DB 21; Local Similarity 64.1%; Pred. No. 9.9e-108; les 963; Conservative 4; Mismatches 494;
                                                                                                                                                                                                                                                                                                                                                                           immunoaffinity chromatography.
                                                                      Claim 1; Page 9; 60pp; English.
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CCGGTTCTACATCGCAGAGCTGACTTTGGCCATTGAGAGTGTCCACAAGATGGGCTTCAT 865
                                                                                                                                                  GAGCCATGTCAGACAGGACAGCATGAGGAGCCCAGCGACCTCTGGGATGATGTGTTGTAACTG
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                                       CCACCGAGACATCAAGCCTGATAACATTTTGATACATCTGGATGGTCACATTAAACTCAC
                                                                               CGACTTTGGCCTGTGCACGGGATTCCGATGGACGCACAACTCGAAGTACTACCAGGAGA-
                                                                                           CCTGGCCCACTCGCTGGTGGGCACCCCGAACTACATAGCTCCCGAGGTGCTGGAGAGRAG
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                                                                                                                                   ----ACGGCAATCACTCGCGCCAGGACTCGATGGAGCCCTGGGAGGAATACTCCGA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAI71765 standard; DNA; 3533 BP.
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sequence is the coding sequence for human cancer-inhibiting Lats2 is a kinase and can be used for gene diagnosis of
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                                                                                                                                                                                                                                                                                                                                                                                                                   42;
                                                                                                                                                                                                                                                                                                                                                                               Length 3533;
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                                                                                                                                                                                                                                                                                                                                            Sequence 3533 BP; 831 A; 1096 C; 1011 G; 595 T; 0 other;
                                                                                                                                                                                                          Novel human Lats2 gene useful for diagnosing cancer
                                                                                                                                                                                                                                                                                                                                                                             Score 557; DB 22;
Pred. No. 1.3e-107;
4; Mismatches 494;
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                                                                                                     IGAKU SEIBUTSUGAKU KENKYUSHO
NOJIMA H.
                                                                                                                                                                                                                                            Claim 1; Page 17-18; 34pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                9.7%;
ilarity 64.1%;
Conservative
                                  18-FEB-2000; 2000JP-0041818
                                                                    .8-FEB-2000; 2000JP-0041818
                                                                                                                                                    WPI; 2001-650995/75.
P-PSDB; AAG78992.
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Best Local Similarity
Matches 963; Conserv
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28-AUG-2001
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(NOJI/)
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7;

Marken JS;

Anderson DM,

Bird TA,

GD,

99WO-US17630 98US-0095270.

Location/Qualifiers 2..1498 /\*tag= a /product= "kinase"

sapiens.

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(IMMV ) IMMUNEX CORP
                                                                                                                                                                                      WPI; 2000-195584/17.
                                                                                                                                                                                                P-PSDB; AAY69160.
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11-SEP-1998;
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2301 CCGGTTCTACATCGCAGAGCTGACTTTGGCCATTGAGAGTGTCCACAAGATGGCTTCAT 2360
                                    GGGTCAGCCGCCCTTCTGGCCAACAGTCCGCTGGAAACGCAACAAAAGGTCATCAACTG 4011
                                                                                                                                                                                                                                                                2781 GGAGAACACGCTCCACATTCCAGCCCAGGTGAAGCTGAGCCCTGAGGCCCAGGGACCTCAT 2840
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                                                                                                                                                                                                                                                                                                                                                                           3021 AAGCCCTTGGAACGATGCCAGCGAAGGTAGCACCAAAGGCCTGGGACACACTCACCTCGCC 3080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kinase activity; molecular weight marker; isoelectric focusing marker; peptide fragmentation control; cellular signal transduction; ss.
                                                               CGACTTTGGCCTGTGCACGGGATTCCGATGGACGCACAACTTCGAAGTACTACCAGGAGA- 3722
                                                                                                                                         ---GAACGGACCGAAGCCCACCGTGCTGGAGAGGCGACGGATGCGCGATCACCAAAGAGT 3831
                                                                                                                                                                             CCTGGCCCACTCGCTGGTGGGCACCCCGAACTACATAGCTCCCGAGGTGCTGGAGAGRAG 3891
                                                                                                                                                                                                                 TGGGTACACGCAGCTGTGCGACTACTGGAGCGTGGGCGTCATCCTYTAYGAGATGCTGGT 3951
                                                                         TCGGTGTGGGGACAGGCTGAAGACCCTAGAGCAGAGGGCGCGGGAAGCAGCACCAGAGGTC
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                            GGAGAAAACSCTGCATATTCCGCCGCAGGCCGAGTTATCCCGCGAGGCTACGGACTTGAT
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                                                                                                    ----ACGGCAATCACTCGCGCCAGGACTCGATGGAGCCCTGGGAGGAATACTCCGA---
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The present sequence encodes a polypeptide which has kinase activity. The kinase polynucleotides can be used to express the polypeptides, and as probes to identify nucleic acids encoding proteins having kinase activity. The kinase polypeptides and fragmented polypeptides are used as molecular weight and isoelectric focusing markers, and as controls for peptide fragmentation. They also have a number of therapeutic uses as kinases play a central role in cellular signal transduction. The polypeptides could also be used to identify binding partner proteins. The polypeptides can also be used as a reagent to identify any proteins that the polypeptide regulates, and proteins with which it might interact. The polypeptides may also be used for preparation of antibodies. The antibodies can be used in assays to detect the presence of the protein, and to purify the protein
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New human kinase polypeptides and polynucleotides used as molecular weight markers and as controls for peptide fragmentation
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Pred. No. 2.4e-103;
                                                                                                     60pp; English.
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                                                                                                     Claim 1; Page 8-9;
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Best Local S
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DNA encoding novel central nervous system protein #37

(first entry)

05-JUN-2002

ABK43457;

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3244 CAAACTGAAGCCCATTGGAGTGGGTGCATTTGGCGAGGTAACGCTGGTGAGCAAAATCGA
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                                                    TACCTCGAACCATTTGTATGCGATGAAAACCCTGCGGAAAGCGGACGTTCTCAAGCGGAA
                                                                  GGTGAAGTTGTACTACAGCTTCCAGGACAAGGATAATCTGTACTTTGTGATGGACTACAT
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hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemla; andiogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemla; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; food additive; food preservative; gene therapy; gene; ss.
system; CNS; autoimmune disease; rheumatoid arthritis;
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2000US-0231413

BP

ABK43457 standard; cDNA; 1912

RESULT 13
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The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded (by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. anjoquenesis, nervous system disorders e.g. Alzheimer's disease and amylotrophic lateral sclerosis, infections caused by bacteria, viruses c.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. denocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukamia, disorders involving neovascularisation e.g. malignancies, crespiratory disorders e.g. nonallargic rhinitis, renal disorders e.g. malignancies, crespiratory disorders en also be used to aid wound healing and ceptrhellal cell proliferation, to prevent skin aging due to subburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to respectate tissues and in chemotaxis. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,
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Pred. No. 4e-103;
4; Mismatches 427; Indels 33;
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Best Local Similarity 65.5%;
Matches 882; Conservative
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                                                                  AAAGCGGACGTTCTCAAGCGGAATCAGGTGGCACACGTGAAGGCCGAGAGGGATATCCTC
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                                 241 GTGTGCCTTGCTTGTAAGGTGGA---CACTCACGCCCTGTACGCCATGAAGACCCTAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence encodes a mouse large tumour suppressor m-lats protein, and has been isolated from a newborn mouse brain phage lambda-ZAP CDNA library using a 2.2-kb DNA probe from the Drosophila lats gene (AAT4117). A homologous mouse sequence has also been isolated (m-lats2, AAT42120). The gene encodes a putative protein-serine/threonine-kinase, and inhibits cell proliferation and plays a crucial role throughout development. Activators or inhibitors of lats function (e.g. an antisense oligonucleotide or dominant-negative lats fragment) may be used in therapy of cancer or other proliferative disorders, degenerative disorders, trauma, growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 deficiency, etc., and fragments of the gene may be used as diagnostic probes. A lats-inhibitor sequence may be expressed in a transgenic plant or farm animal to confer increased growth and inhibit
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enhancing proliferation
                                                                                                                                                                                                                                                                                                                               protein-serine/threonine-kinase; cell proliferation; antisense; dominant-negative; cancer; degenerative disorder; trauma; growth deficiency; therapy; antitumour; vulnerary; diagnostic;
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es 421;
                                                                                                                                                                                                                                                                                                             m-lats gene; large tumour suppressor;
                                                                                                                                                                                                                                                                 M-lats gene encoding large tumour suppressor.
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The present sequence is a DNA encoding mouse Lats (large tumour suppressor) protein which is a cell overproliferation inhibitor and a negative regulator of cell cycle-dependent kinase do2/Cyclin A. The present sequence is useful for treating cancer that is refractory to standard chemotherapy or radiation therapy such as hyperplasia, to syplasia, and disorders associated with aberrant levels of cdc2 activity. Conditions treated by promoting cdc2 function include degenerative disorders, growth deficiencies, hypoproliferative disorders, physical trauma, lesions, and wounds. An animal model preferably a mouse, in which a lats gene has been disrupted by homologous recombination, e.g. a lats knock-out mouse, is used for screening compounds that can be used to treat or prevent cancer, particularly
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skin cancer, soft tissue sarcomas and ovarian tumours, and disorders associated with pituitary dysfunction e.g. luteinizing hormone (LH) hypogonadotropic hypogonadism. The lats DNA is also used in gene therapy.
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                                                                                                                                                                                              3044 AAGTICTICATGGAGCAGCACATAGAGAACGTGATCAAGTGGTATGGCCAGGGCACGTAT 3103
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                                                                                                                     27;
                                                                                           Length 3213;
                                                                                     Score 522.8; DB 21; Length
Pred. No. 2.1e-100;
4; Mismatches 421; Indels
                                                     Sequence 3213 BP; 946 A; 764 C; 696 G; 807 T; 0 other;
                                                                                     9.1%;
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                                                                                                 Similarity
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                ACGCAACAAAAGGTCATCAACTGGGAGAAAACSCTGCATATTCCGCCGCAGGCCGAGTTA
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Search completed: January 16, 2003, 10:36:52 Job time : 895.592 secs

Sequence 48, Sequence 24, Patent No. 52 Sequence 1,

Sequence

Sequence

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Sequence

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APPLICANT: Wang, Weiyi
APPLICANT: Zhang, Sheng
APPLICANT: Zhang, Sheng
APPLICANT: Yu, Wang
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS
TITLE OF INVENTION: GENES AND METHODS BASED THEREON
CORRESPONDENCE: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/442,100
 US-09-230-371A-20

US-08-685-571-1

US-09-313-930-1

US-09-212-771-1

US-09-091-058-1

US-08-966-316-10

US-09-289-466-1

US-09-289-466-1

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                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEE: Pennie & Edmonds
: 1155 Avenue of the Americas
New York
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/411,111
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09442100 Patent No. 6359193 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
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TELECOMMUNICATION INFORMATION:
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APPLICANT: Tao, Wufan
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LOCATION:
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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2: //cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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1140 1200 1260 1200 1260 1320 1320 1380 1380 1440 1440 1500 1500 1560 1560 1620 1680 1740 1800 1920 1800 1860 1860 1980 2100 TGATAAATACACGGCGGAAGCCCTCGAGGCATCAAGCAGGACCTAACCCGATTTGAAGT ACAAAATAACCATAGGAATAATCAGAATTACACACCTCTGCGATACACGGCGACCAACGG **ACGCAACGATGCACTTACTCCTGACTATCACCACGCCAAGCAGCCGATGGAGCCGCCACC** CTCCGCCTCTCCTGCTCCGGACGTGGTCATACCGCCGCCGCCGCCGCTTTGTAGGTCAGCC CGGAGCCGGCTCCATATCCGTATCCGGTGTGGGCGTTGGAGTGGTGGGGTGTGGCGAACGG CGAACGGGACACGGCGAGCAGTCACTACCTGCGCTGCAGTCCGGGCTCTGGACTCCGGAGC 1501 CGAACGGGACACGGCGAGCAGTCACTACCTGCGCTGCAGCCCGGCTCTGGACTCCGGAGC ACGTGTSCCAAAGATGATGACGGCCCTAATGCCAAACAAACTGATCCGGAAGCCGAGCAT GGCTCCACCGGCGCCGCCACGCAATCCCACGCCTSCAGCGCGGCCACGCCCCCACC GCCAGTGCCGCCCACCAGCCAGGCGTAACGTGAAGCGGCGATCACCGGCCCTGAACAACCG GGTGGGTAATCCAGGTGGAAATGGTGGATTTTCTCCGTCGCCAAGCGGTTTCAGTGAGGT GCTGAAGAACCCGCAGCAGCAGTTGACGCAGCTGAAGTCCCTGAACCTATACCCAGG CGGAGGCAGTGGAGCAGTKGTGGAGCCACCGCCCCTACCTAATTCAAGGCGGAGCCGG AGGAGCAGCACCGCCGCCACCACCACCACGACTACCACGCCTCCATGCAGTCGCGGCAGTC 1201 1261 1441 1441 1021 1021 1081 1081 1141 1141 1201 1261 1321 1321 1381 1381 1681 1501 1561 1561 1621 1621 1681. 1741 1741 1801 1801 1861 1861 1921 1921 1981 1981 2041 2041 q g ŏ Ω ò q Qγ g Qy g δy Q g δ a δ ò qq ò 셤 οy g qq qq  $^{\circ}$ οy g δ ò g δy a ò Db QYqq

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	CACCTCGGCGGGCTCGCCGAGCCCCATAACTGTGTCSCTGCCGCCGGCGCCGCTGGCGAA	2161 GCGACAACCACGAGTCTACCAGGCCAGGAGTCAGCCGATCATCATGCAGAGTGTGAA 2220 2221 GAGCACĠCAGGTCCAAAAGCCGTGCTGCAAACAGCAGTGGCGCGCCAATCGCCATCGAG 2280 11111111111111111111111111111111111	2281 TGCCTCGCCAGCAATTCACCAGTCCACGTGGCGGCTCCACCCTCTTACCCTCAGAA 2340	AGCA 240       AGCA 240	AYAG  :   ACAG		GCTGGTARAGCAGCAGCAGCAGCAGCARCARCAGCAGGTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	ACAGCAGCAGCARCAACAACAACAACAACTGCAGGCCTTGAGGTGCTCCAGGCACAGGC 264	TCAGAGGGAGCGGGATCAACGGGAGCGGGAACGGATCAGCAGAGGTGCTCCAGGCACGGAACGGAACGGAACGGGAACGGGAACGGGAACGGGAACGGGAACGGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGCAAACGCAAACGCAAACGCAAACGAAAACTGACAAAACGTGACAAACGCAAAACGTAAAACTGAAAACGTGAAACGAAAA 270	TCTGGCCGGCAGATGCTTCCGCCGCCCTATCAGAGCAACAACAACAACAACGG 27 TCTGGCCGGCAGATGCTTCCGCCGCCCCTATCAGAGCAACAACAACAACAACAACAACAACAACAACAACA	GATCABACCGCCGACCACACAACAACATAACATAAGAACAACAACAACAACAACAACAACAACAACAACAACA	GACACCACCATTCCGCCTGCCAAATACAATAACAACTCCTCCAACACGGGCGCGAATAG	CTCGGGCGGCAGCAACGGATCCACCGCCACCGCCTCCTCGTCGACCAGCTGCAAGAA		GCGCAAGGAGTTCCGCATCAGGCAGTACTCGCCGCAAGCCTTCAAGTTCTTCATGGGGGAACGAAGGAGTTCCTCATGATACTCGCCGCAAGGCTTCAAGTTCTTCATGAGGAGCAAGGAAGG		GAAGGAGATGCACAAAGTGGGACTGCCCGATCAGACCCAAATCGAGATGAGGAAAAATGCT [	GAACCAAAAGGAGAGCAACTACATTCGATTGAAGCGCCCAAGATGGACAAGATGTT

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131   TITICGAATTACCTTCCCGCCGCCACACACACACCCCCGCACATTACACCGCACCACATTACACCGCCCCCCCC	Ov 5401		Oy . 5461	Db 5461 Qy 5521 Q		OY 5581.	Oy 5641	Db 5641		RESULT 2 US-09-442- ; Sequence	GENERAL GENERAL APPL	APPL: APPL: TITLI	CORRI	ST	COMP	SO CURR P AP	CL PRIO PRIO PRIO	ATTO NA RE	TELE	SEQUAL SEQUE	ST TC TC TC
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	Db 4261	4	Db 4321	Qy 4381 Db 4381			Db 4501						4 4	4 4	4 4						

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NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS GENES AND METHODS BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OFTWARE: PATEMTIN Release #1.0, Version #1.30
APPLICATION DATA:
OPPLICATION NUMBER: US/09/442,100
                                                                                                                                                                                                                                                                                                                                                                                                   LICANT: Wang, Weiyi
LICANT: Zhang, Sheng
LICANT: Yu, Wan
LIE OF INVENTION: UNCLEOTIDE AND PROTEIN
LIE OF INVENTION: GENES AND METHODS BASED
LIBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1: Pennie & Edmonds
1155 Avenue of the Americas
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LASSIFICATION:
OR APPLICATION DATA:
PPLICATION NUMBER: 08/411,111
                                                                                                                                                                                                                                                                                                                                            De 7, Application US/09442100
No. 6359193
NI INFORMATION:
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(212) 869-9741/8864
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REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 652
ECOMMUNICATION INFORMATION: (212) 790-9090
                                                                                                                                                                                                                                                                      GCCTTGGCCAATTAGTTTAC 5720
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CICANT: Tao, Wufan
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es 491;
                                                               Pred. No. 6.864; Mismatches
                                                     Score 567.8;
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ilarity 64.3%;
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                 ; LOCATION:
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                          GAGCGTGGACGAGGTCAAGAGCCACGACTTCTTCAAGGGCATCGACTTTGC---GGACAT
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APPLICANT: Bird, Timothy A.
APPLICANT: Anderson, Dirk M.
APPLICANT: Marken, John S.
TITLE OF INVENTION: Human cDNAs Encoding Polypeptides I FILE REFERENCE: 2877-US
CURRENT APPLICATION NUMBER: US/09/509,902A
CURRENT FILIKO DATE: 1999-08-03
NUMBER OF SEQ ID NOS: 16
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Pred. No. 2e-123
4; Mismatches 4
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US-09-509-902A-15
: Sequence 15, Application US/09509902A
; Patent No. 6387676
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Matches 963; Conservative
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APPLICANT: VICCA, I
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LENGTH: 1961
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Human cDNAs Encoding Polypeptides Having Kinase Functions 4072 AAGGAGGCTCTGTGCGTCGGCTGGGCTGGGCAAGAGCGTGGACGAGG---TCAA 4128 GAGCCACGACTTCTTCAAGGCCATCGACTTTGC---GGACATGCGGAAGCAAAAGCGCC 4185 4245 1466 CTACGTTCCCACCATCAGCCACCCATGGACACCTCGAATTTCGACCCGTAGAAGA 1525 1526 AAGCCCTTGGAACGATGCCAGCGAAGGTAGCACCAAGGCCTGGGACACACTCACCTCGCC 1585 4353 --GA 4293 2944 CAAGCACGCCTCGCCCATCCCGGAGCGCAAGAAGATCTCCAAGGAGAAGGAGGAGGAGCG 3003 2884 GGGCGGCAGCAACGGATCCACCGGCACCACCGCCTCCTCGTCGACCAGCTGCAAGAAGAT 2943 3004 CAAGGAGTECGGATEAGGCAGTACTEGECGCAAGCCTTCAAGTTCTTCATGAGCAGCA 3063 CCAAAAGGAGAGCAACTACATTCGATTGAAGCGCGCCAAGATGGACAAGAGCATGTTCGT 3243 220 GATTCAGACCTCTCCCGTTCCCGTCCGCAAAACAGC.-----AGAGACGAAGAGA 270 4186 CTACATACCGGAAATCAAGCACCCRACGGACACATCCAACTTTGATCCCGTGGATCCGGA 4294 CCAGAATGACCGCACYTTCCACGGCTTTTTCGAATTTACCTTCCGTCGCTTCTTCGACGA 271 GAGAGAGTCACGCATCAĞGAGCTACTCGCCATTAAGTTCTTCATGGAGCAGCA 3064 CATAGAGAACGIGAICAAGICGIAICGCCAGCGCACGIAICGCAAGAAICAGCIGGAGAA GGAGATGCACAAAGTGGGACTGCCCGATCAGACCCAAATCGAGATGAGGAAAATGCTGAA 30; Length 1498; Score 536, DB 4, Length 14 Pred. No. 1.8e-118, 3; Mismatches 433; Indels 4246 GAAGCTGCGCTCGAATGACTCCACCATGAGCAGCGGCGATGATGTC-APPLICANT: Marken, John S.
TITLE OF INVENTION: Human cDNAS Encoding
FILE REFERENCE: 2877-US.
CURRENT APPLICATION NUMBER: US/09/509, 902A
CURRENT FILLS DATE: 1999-08-03
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentr. V.-Sequence 6, Application US/09509902A Patent No. 6387676 Query Match
Best Local Similarity 65.5%;
Matches 884; Conservative Virca, Duke Bird, Timothy A. Anderson, Dirk M. ; ORGANISM: Homo sapiens US-09-509-902A-6 GENERAL INFORMATION: 4354 CAA 4356 1646 CAA 1648 US-09-509-902A-6 1498 TYPE: DNA APPLICANT: SEQ ID NO 6 LENGIH: 14 APPLICANT: 4129 3184 3124 391 451 RESULT 4 οy g ò Dp δŏ qq Oy g g Ω g δλ g ŏ Pp qq ò

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GENERAL INFORMATION:
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3244 CAAACTGAAGCCCATTGGAGTGGGTGCATTTGGCGAGGTAACGCTGGTGAGCAAAAATCGA 3303
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                  ---CACTCACGCCCTGTACGCCATGAAGAACGAAAAAGGATGTCCTGAACCGGAA
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                                                                  3304 TACCTCGAACCATTTGTATGCGATGAAAACCCTGCGGAAAGCGGACGTTCTCAAGCGGAA
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3044 AAGTICTICATGGAGCAGCACATAGAGAACGTGATCAAGTCGTATCGCCAGCGCACGTAT 3103
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                                                                                   OF LATS
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                                                                                                GENES AND METHODS BASED THEREON
                                                                                                                                                                                                                                                                                                  SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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Pred. No. 4e-115;
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                                                                                 NUCLEOTIDE AND PROTEIN
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                                                                                                                                                 1: Pennie & Edmonds
1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/411,111
                                                                                                                                                                                                                          ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (212) 790-9090
(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 65
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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APPLICANT: Xu, Tian
APPLICANT: Tao, Wufan
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                                                APPLICANT: Zhang, SPAPLICANT: Yu, Wan TITLE OF INVENTION: TITLE OF INVENTION:
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                                                                                                                                                                                                   New York
                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                   New York
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TOPOLOGY: unk
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; LOCATION:
US-09-442-100-5
                               APPLICANT:
APPLICANT:
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Best Local
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; Sequence 5, Application US/09442100

US-09-442-100-5

RESULT 5

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                         1654 TGTCTAGCAAGAAAAGTCGATA --- CTAAAGCTTTGTATGCAACAAGACTCTTCGAAAG 1710
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                                                    GCGGACGTTCTCAAGCGGAATCAGGTGGCACACGTGAAGGCCGAGAGGGATATCCTCGCG
                                                                   GAAGCCGACAATAACTGGGTGGTGAAGTTGTACTACAGCTTCCAGGACAAGGATAATCTG
                                                                                                                      TACTTIGIGATGGACTACATACCAGGTGGTGATCTGATGTCGCTGCTCATCAAACTGGGC
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US-09-442-100-3
; Sequence 3, Application US/09442100
; Patent No. 6359193
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3284 ACGCTGGTGAGCAAAATCGATACCTCGAACCATTTGTATGCGATGAAAACCCTGCGGAAA 3343

ATGGACAAGTCTATGTTTGTGAAGATAAAGACACTAGGAATAGGAGCATTTGGTGAAGTC 2387

2328

3224 AIGGACAAGAGCAIGTICGICAAACIGAAGCCCAIIGGAGIGGGIGCAITIGGCGAGGIA

2268 CAAATGAGAAAGATGCTTTGCCAAAAAGAATGTAACATGCGTCTTAAAAGGGCTAAA 2327

3044 AAGTICTICAIGGAGCAGCACAIAGAGAACGIGAICAAGTCGIAICGCCAGCGCACGIAI 3103

CGCAAGAATĊAGCTGGAGAAGGAGGATGCACAAAGTGGGACTGCCCGATCAGACCCAAATC 3163

3104

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2208 CGTAAAAACAATTAGAGAATGAAATGATGCGGGTTGGATTATCTCAACATGCCCAGGAT 3164 GAGATGAGGAAAAATGCTGAACCAAAAGGAGGGCGCGAGG 3283

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2088 AACAAGAAAGATGAAGAGAATCTCGTATTCAAAGTTATTCTCCTCAAGCATT 2147
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                                                  NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS GENES AND METHODS BASED THEREON
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Pred. No. 1.4e-102;
4; Mismatches 453;
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                                                                                                                                        1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/411,111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (212) 869-9741/8864
                                                                                                                                                                                                                                                     IBM PC compatible
                                                                                                                         Pennie & Edmonds
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
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Best Local Similarity 62.8
Matches 817: Conservative
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US
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231..3623
                                                                                                         CORRESPONDENCE ADDRESS:
               Wang, Welyl
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                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                         TITLE OF INVENTION:
                                                                                                                                                                         New York
                                                                                                                                                                                       RY: USA
10036-2711
                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                          New York
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US-09-442-100-3
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                                               APPLICANT:
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Steinmann, Kathleen E. Astle, Jon H.

Burgess, Christopher C Bushnell, Steven E. Carroll III, Eddie Catino, Theodore J. Derti, Adnan

Lewis, Marcia E. Monahan, John E. Schlegel, Robert

Ford, Donna M.

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TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION FILL OF INVENTION: PRODUCTS
FILL REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 850
                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                      US-09-328-111-26
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APPLICANT: C
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2388 TGTCTAGCAAGAAAAGTAGATA---CTAAGGCTTTGTATGCAACAAAAACTCTTCGAAAG 2444
                                                     ATTTTCGAGGAGGAACTGGCCAGATTCTACATCGCCGAGGTCACCTGCGCCGTGGACAGC 3583
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                                                                                           GAAGCCGACAATAACTGGGTGGTGAAGTTGTACTACAGCTTCCAGGACAAGGATAATCTG
                                                                                                                                              TACTITGTGATGGACTACATACCAGGTGGTGATCTGATGTCGCTGCTCATCAAACTGGGC
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US-09-328-111-26/c
; Sequence 26, Application US/09328111
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Score 273.6; DB 4;
Pred. No. 6.4e-56;
0; Mismatches 209;
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Best Local Similarity 66.4%;
Matches 425; Conservative
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3640 TAGGGACGGACACATAAAGCTCACCGACTTTGGCCTGTGCACGGGATTCCGATGGACGCA 3699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER:
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LOCATION: (13
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US-09-338-132-1
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SOFTWARE:
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                                                                                                                                                                                             APPLICANT: Millward, Thomas A.
TITLE OF INVENTION: Nuclear DBF2-Related (NDR) Kinases
FILE REFERENCE: 4-20265/A/PCT
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      GGCCTCTGCACTGGCTTCAGATGGACACACGATTCTAAGT
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Pred. No. 1.1
                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: PCT/EP95/05052
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: 94810746.1
EARLIER FILING DATE: 1994-12-22
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/08/860,150B
CURRENT FILING DATE: 1997-06-19
                                                                                                        Sequence 1, Application US/08860150B Patent No. 5981205
GENERAL INFORMATION:
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; LOCATION: (132)..(1499)
US-08-860-150-1
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Matches 581; Conserv
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LENGTH: 2101
                                                                   RESULT 8
US-08-860-150-1
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                                                            3700 CAACTCGAAGTACTACCAGGAGAACGGCAATCACTCGCGCCAGGACTCGATGGAGCCCTG
                                                                                                           869 TCGAACATTTTATCGGGACTTGTCGCGAAACCATCCGTTTTATAGGCACGTG
                                                                                                                                                                                              3760 GGAGGAATACTCCGAGAACGGACCGAAGCCCCACCGTGCTGGAGAGGCGACGGATGCGCGA
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809 CGCGCGAGGGCATCTGAAGCTCTCCGACTTCGGACTGTGCACTGGCTTAAAGAAGTCGCA
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TITLE OF INVENTION: .Nuclear DBF2-Related (NDR) Kinases
FILE REFERENCE: 4-20265/A/PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 261.2; DB 3;
Pred. No. 1.1e-52;
3; Mismatches 451;
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EARLIER APPLICATION NUMBER: 08/860,150
EARLIER FILING DATE: 1997-06-19
EARLIER FILING DATE: 1997-06-19
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: 94810746.1
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ORGANISM: Drosophila melanogaster
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Ayad-Durieux, Yasmina

Dietrich, Fred

PatentIn Ver. 2.0

2160

gossypii

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APPLICANT: Philippsen, Peter
TITLE OF INVENTION: Fungal Target Genes and Methods
FILE REFERENCE: PB/5-30908A
CURRENT APPLICATION UNMBER: US/09/588,256
CURRENT FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                          ; LOCATION: (1)..(2160)
US-09-588-256-1
                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Ashbya
                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
                       APPLICANT:
APPLICANT:
APPLICANT:
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CGAGATGAGGAAAATGCTGAACCAAAAGGAGGAACTACATTCGATTGAAGCGCGCCAA 3222
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                                   332 GGAGAAGCGTCTGCAGCATGCCCAGAAGGAGGAGGGAGTATCTCCGGCTGAAGCGATTGCG
                                                                                                           392 CCTCGGTGTGGAGGACTTTGAGGCCCTCAAAGTCATCGGACGCGGCGCGTTCGGTGAAGT
                                                                                                                                                   AACGCTGGTGAGCAAAATCGATACCTCGAACCATTTGTATGCGATGAAAACCCTGCGGAA
                                                                                                                                                                                    GCGTTTGGTGCAGAAAAGGACACTGG---ACATGTGTGCGCCATGAAGGTGCTGCGCAA
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                                                                  3179 CTGAACCAAAAGGAGAGCAACTACATTCGATTGAAGCGCGCCAAGATGGACAAGAGCATG 3238
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                                     :99
 Length 2160;
                   .9e-51;
                                  2; Mismatches
Score 254.8;
Pred. No. 3.9
Query Match 4.5%;
Best Local Similarity 55.0%;
Matches 626; Conservative
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Sequence 1, Application US/09588256 Patent No. 6291665

us-09-588-256-1

RESULT 10

GENERAL INFORMATION:

APPLICANT:

APPLICANT: APPLICANT:

Gaffney, Thomas

Albert

Gates, Krista Flavier,

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                                                                                                                                                                                                                                                                                                                 1945 AAGCTGTCCAGGGTCACGACAGGGGGTTCCCAACAGAGGTGGAGAAGCTGGAGAAGGTGC 2002
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                                              CCGCCCTTTCTGGCCAACAGTCCGCTGGAAACGCAACAAAAGGTCATCAACTGGGAGAAA
                                                                                                                                      ACSCTGCATATTCCGCCGCAGGCCGAGTTATCCCGCGAGGCTACGGACTTGATAAGGAGG
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APPLICANT: Hounings, Thomas A.
TITLE OF INVENTION NUCLEAR DBF2-Related (NDR) Kinases
TITLE OF INVENTION NUCLEAR DBF2-Related (NDR) Kinases
CURRENT FILING DATE: 1997-06-19
EARLIER FILING DATE: 1997-06-19
EARLIER FILING DATE: 1995-12-20
EARLIER FILING DATE: 1995-12-20
EARLIER FILING DATE: 1994-12-22
NUMBER: PAPLICATION NUMBER: 94810746.1
EARLIER FILING DATE: 1994-12-22
NUMBER: PALENTION NUMBER: 94810746.1
SOFTWARE: PALENTIN VOICE: 20
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Pred. No. 9.6e-46;
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08860150B Patent No. 5981205
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; LOCATION: (596)..(1990)
US-08-860-150-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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\*\*RESULT 12
US-09-338-132-6
Sequence 6, Application US/09338132
Patent No. 6040164
GENERAL INFORMATION:
APPLICANT: Hemmings, Brian A.
APPLICANT: Milward, Thomas A.
TILE REFERENCE: 4-20265/A/PCT
CURRENT PAPLICATION NUMBER: US/09/338,132
CURRENT FILIG DATE: 1999-06-22
EARLIER APPLICATION NUMBER: 08/960,150

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PF-0321 US
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Goli, Surya K.
Shah, Purvi
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SEQUENCE CHARACTERISTICS:
LENGTH: 1935 base pairs
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Pred. No. 9.6e-46;
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              EARLIER APPLICATION NUMBER: PCT/EP95/05052
EARLIER FILING DATE: 1995-112-20
EARLIER PLICATION NUMBER: 94810746.1
EARLIER FILING DATE: 1994-12-22
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
EARLIER FILING DATE: 1997-06-19
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US-09-272-796-11
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                                                                                                        Length 1935;
                                                                                                                       Pred. No. 5.1e-42;
2; Mismatches 556; Indels
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                                                                                                   Score 216.6; DB 2;
                                                                                                   3.8%;
                                                                                                                                              Matches 609; Conservative
LIBRARY: SYNORATO4
CLONE: 705365
                                                                                                                            Similarity
                                                US-08-878-989-11
                                                                                                Query Match
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4120 CGAGGTCAAGAGCCACGACTTCTTCAAGGGCATCGACTTTGCGGACATGCGGAAGCAGAA 4179
                                     1114 GGACTTAATTCTCAGATTTTGTATTGATTCTGAAAACAGAATTGGAAATAGTGGAGTAGA 1173
                                                                                                       Gaps
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                                                                                                                                                                                   4063.GGACTTGATAAGGAGGCTCTGTGCGTCGGCTGACAAGCGGCTGGGCAAGA---GCGTGGA
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Pred. No. 5.1e-42;
2; Mismatches 556;
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                                                                                                                                                                                                                                                                                                Sequence 11, Application US/09272796
Patent No. 6207148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                Hillman, Jennifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                       Guegler, Karl G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM Compatible
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Shah, Purvi
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LENGTH: 1935 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              URRENT APPLICATION DATA
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Matches 609; Conservative
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EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
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3438 ACAGCTTCCAGGACAAGGATAATCTGTACTTTGTGATGGACTACATACCAGGTGGTGATC 3497
                                                                                                                                                                                                                                                                               Burgess, Christopher
Bushnell, Steven E.
Carroll III, Eddie
Catino, Theodore J.
                                                                                                                                                                                                                             APPLICANT: Endege, Wilson O. APPLICANT: Steinmann, Kathleen APPLICANT: Astle, Jon H.
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Best Local Similarity 63.2%;
Matches 285; Conservative
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                                                                                                                                                                                                                                                                                                                                                      Derti, Adnan
Ford, Donna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
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                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                      CGAGATGAGGAAAATGCTGAACCAAAAGGAGGAGCAACTACATTCGATTGAAGCGCGCCAA 3222
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                                CAAGCTCACATTGGAGAATTTTTATAGCAACCTAATTTTACAGCATGAAGAGAGAAAC
                                                                   3103 TCGCAAGAATCAGCTGGAGAAGGAGGATGCACAAAGTGGGACTGCCCGATCAGACCCAAAT
                                                                                                                                                                        GTTACGTCGATCACACACGCTCGCAAAGAAACAGAGTTCTTACGGCTCAAAAGGACCAG
                                                                                                                                                                                                         GATGGACAAGAGCATGTTCGTCAAACTGAAGCCCCATTGGAGTGGGTGCATTTGGCGAGGT
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TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 164.6; DB 4;
Pred. No. 7.7e-30;
0; Mismatches 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: CCD-557 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER TILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PSECISE OF Windows Version 3:0
                                                                                                                                                                                                                                                        Application US/09328111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTHER INFORMATION: n = A,T,C or US-09-328-111-66
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Search completed: January 16, 2003, 21:59:35 Job time: 245.379 secs

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GenCore version 5.1.3

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OM nucleic - nucleic search, using sw model

Run on: January 16, 2003, 09:56:42; Search time 158.731 Seconds

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16067.254 Million cell updates/sec

Title:
105-09-763-334-7

Sequence: 105-09-763-334-7

Sequence: 105-09-763-334-7

Sequence: 105-09-763-334-7

Scoring table: 105MTTY_NUC

Gapop 10.0, Gapext 1.0

Searched: 393868 seqs, 222934149 residues

Total number of hits satisfying chosen parameters: 787736

Minimum DB seq length: 0

Maximum Match 100

Maximum Match 100

Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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pubpna/US08\_PUBCOMB.seq: pubpna/US09\_NEW\_PUB.seq: /pubpna/US09\_PUBCOMB.seq

/pubpna/USO7\_NEW\_PUB.seg /pubpna/PCTUS\_PUBCOMB.seg /pubpna/USO8\_NEW\_PUB.seg

Published\_Applications\_NA:

Database :

/cgn2\_6

## UMMARIES

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Result No.	ult No.	Score	Ma	Query Match	Query Match Length	DB	ID	Description
:		487.8		. 2.	2043	. 6	US-09-836-392-2	Sequence 2, Appli
	7	321.4		5.6	949	6	US-09-764-868-214	Sequence 214, App
υ	æ	273.6		4.8	638	10	US-09-879-536-26	Sequence 26, Appl
	4	232.6		4.1	3583	6	US-09-974-298-152	Sequence 152, App
	Ŋ	200.6		3.5	1452	6	US-09-938-842A-2402	Sequence 2402, Ap
	9	195.8		3.4	1689	6	US-09-938-842A-1861	Sequence 1861, Ap
	7	188.6		3,3	1818	10	US-09-771-161A-89	Sequence 89, Appl
	æ	164.6		2.9	678	10	US-09-879-536-66	
	0	161.2		2.8	734	6	US-09-764-868-196	
	10	144.6		2.5	1398	σ	US-09-938-842A-633	m
	11	138.6		2.4	. 1416	σ	US-09-938-842A-2503	'n
	12	134.6		2.4	3061	10	US-09-880-107-2146	Sequence 2146, Ap
	13	134.6		2.4	3407	10	US-09-971-845-1	Sequence 1, Appli
	14	133		2.3	362	σ	US-09-796-692-7789	Sequence 7789, Ap.
	15	127		2.2	1635	10	US-09-880-107-2340	Sequence 2340, Ap
	16	121.8		2.1	1244	10	US-09-771-161A-38	Sequence 38, Appl
	17	121.8		2.1	1393	10	US-09-771-161A-37	
	18	121		2.1	1735	σ	US-09-764-868-58	Sequence 58, Appl
	19	120.6		2.1	2549	10	US-09-880-107-3691	Sequence 3691, Ap

1, 1 113, 1 166, 1 527, 1 1, 1 1, 1 1, 1 204, 1 293, 1	Sequence 63, Appl. Sequence 63, Appl. Sequence 1, Appl. Sequence 3, Appl. Sequence 571, App. Sequence 571, App. Sequence 168, App. Sequence 168, App. Sequence 13, Appl. Sequence 13, Appl. Sequence 1, Appl.
88 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	10 US-09-711-161A-63 10 US-09-711-161A-63 11 US-09-804-471A-1 12 US-10-028-946-3 12 US-10-028-946-1 12 US-10-174-590-571 12 US-10-174-590-571 12 US-10-174-590-571 12 US-10-052-586-571 10 US-09-974-298-168 10 US-09-974-298-168 10 US-09-974-298-168 10 US-09-974-298-168 10 US-09-974-298-168
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## ALIGNMENTS

	RESULT	RESULT 1 IIS-09-836-392-2
	Se	Sequence 2, Application US/09836392
	GE :	FACELL NO. OZZOZOZI 1/450A1 GENERAL INFORMATION:
,	A	APPLICANT: Ruben et al.
		TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypeptides TITLE OF INVENTION: Antibodies
	<u></u>	FILE REFERENCE: PT020P1
		CURRENT APPLICATION NUMBER: US/09/836,392
		CURKENI FILING DATE:
		FRIOR FILING DATE: 2000-10-11
	٠.	
	<u>а</u>	PRIOR APPLICATION NUMBER: 60/165, 914
	٠.	PRIOR FILING DATE: 1999-11-17
		PRIOR APPLICATION NUMBER: 00/189,02/
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	· č	100 Match 0 58. Come 107 0. DB 0. Tomath 2013.
	Be	Query march Best Local Similarity 65.2%; Pred. No. 1.3e-97;
	Wa	tches 819; Conservative 4; Mismatches 401; Indels 33; Gaps 6;
	Οy	3130 GCACAAAGTGGGACTGCCCGATCAGACCCAAATGGAGATGAGGAAAATGCTGAACCAAAA 3189
	qq	
	ΟŊ	3190 GGAGAGCAACTACATTGGATTGAAGCGCGCCAAGATGGACAAGAGCATGTTCGTCAAACT 3249
	qa	271 AGAGTCTAATTACAACAGGTTAAAGAGGGCCCAAGATGGACAAGTCTATGTTTGTCAAGAT 330
	ΟŊ	3250 GAAGCCCATTGGAGTGGGTGCATTTGGCGAGGTAACGCTGGTGAGCAAAATCGATACCTC 3309
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3310 GAACCATTTGTATGCGATGAAAACCCTGCGGAAAGCGGACGTTCTCAAGCGGAATCAGGT
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PAL
NUMBER OF SEQ ID NOS: 1510
SUFWARE: Patentin Ver. 2.0 or n equals a,t,g, AACTCGAAGTACTACCAGGA 3720 7 5.6%; Best Local Similarity 69.7 Matches 474; Conservative Sequence 214, Application Patent No. US20020168711A1 ORGANISM: Homo sapiens COTHER INFORMATION: US-09-764-868-214 GENERAL INFORMATION: NAME/KEY: SITE LOCATION: (628) RESULT 2 US-09-764-868-214 SEQ ID NO 214 Query Match TYPE: DNA ENGTH: 3581 FEATURE 536 3281 3461 3521 477 298 3401 358 417 Ω g ŏλ g ò Op δ g ŏ g g δ Оp QΫ́ g ŏ 원 δλ g Qγ

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                                                                                 ACAAGAGCATGTTCGTCAAACTGAAGCCCATTGGAGTGGGTGCATTTGGCGAGGTAACGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATTGAAGATTTGAGTCCGTAAAAGTAATAGGCAGAGGAGCATTGGTGAGGTACGCC
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; OTHER INFORMATION: Incyte ID No. US20020156263A1 347975.11
US-09-974-298-152
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chen, Huei-Mei
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE: PA-0037 P
CURRENT APPLICATION UNMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR FILING DATE: 2000-05-10
                                                                                                                                    3671 GGCCTGTGCACGGGATTCCGATGGACGCACAACTCGAAGT 3710
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Pred. No. 2.2e-41;
2; Mismatches 496;
                                                                                                                                                          Sequence 152, Application US/09974298
Patent No. US20020156263A1
GENERAL INFORMATION:
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Best Local Similarity 53.1%;
Matches 599; Conservative
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SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                   RESULT 4
US-09-974-298-152
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LENGTH: 3583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3194 AGCAACTACATTCGATTGAAGCGCGCCAAGATGGACAAGAGCATGTTCGTCAAACTGAAG 3253
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                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
AITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
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SOFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
LENGTH: 638
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CURRENT APPLICATION NUMBER: US/09/879,536
CURRENT FILING DATE: 2001-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/088,801
PRIOR FILING DATE: 1998-06-10
                                                                                                               Sequence 26, Application US/09879536
Patent No. US20020144298A1
                                                                                                                                                                                                                               Burgess, Christopher C.
Bushnell, Steven E.
Carroll III, Eddie
Catino, Theodore J.
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Astle, Jon H.
656 AATTCCAATATTACCAGAA 675
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                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Endege, Wilson O.
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Best Local Similarity 66.4
Matches 425; Conservative
                                                                                                                                                                                                                                                                                                                                   Donna M.
                                                                                                                                                                                                                                                                                                                Derti, Adnan
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US-09-879-536-26
                                                                                                                                                                                                                                                                                                                                   Ford,
                                                                                       .09-879-536-26/c
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APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Wang, Yun
APPLICANT: Au, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSCENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
                           GACACATAAAGCTCACCGACTTTGGCCTGTGCACGGGATTCCGATGGACGCACAACTCGA 3707
                                           3767
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                                                                                                                                                                                                                                                                   3948 TGGTGGGTCAGCCGCCTTTCTGGCCAACAGTCCGCTGGAAACGCAAAAAGGTCATCA 4007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCAACTIGGATICATCCACAGAGACATCAAACCAGACAACCTICTITIGGACAGCAAGG 953
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                                                                                AGTACTACCAGGAGAACGGCAATCACTCGCGCCAGGACTCGATGGAGCCCTGGGAGGAAT
                                                                                                         1014 AATTTTA-TAGGAATCTGAACCACGCCTCCCCAGTGATTTCACTTTCCAGAACATGAAT
                                                                                                                                     ACTCCGAGAACGGACCGAAGCCCACCGTGCTGGAGAGGCGACGGATGCGCGATCACCAAA
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                                                                                                                                                              1073 TCCAAAAGGAAAGCAGAAACCTGGAAAAGAAATAGACGTCA------
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Pred. No. 1.5e-34;
3; Mismatches 617;
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PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
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Best Local Similarity 49.6:
Matches 640; Conservative
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                                                        AAGTTCTTCATGGAGCACACATAGAGAACGTGATCAAGTCGTATCGCCAGCGCACGTAT
                                                                                              85 AAGCAGTACATCGAGAATCACTACAAAGCTCAGAACAAGAAAATCAAGAGAAAGAG
                                                                                                                                           CGCAAGAATCAGCTGGAGAAGGAGATGCACAAAGTGGGACTGCCCGATCAGACCCAAATC
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Patent No. US20020110811A1
GENERAL INFORMATION:
APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
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PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
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  AGTTATCCCGCGAGGCTACGGACTTGATAAGGAGGCTCTGTGCGGTCGGCTGACAAGCGGC
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ches 591;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: STRESS-REGULATED GENES OF
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
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Pred. No. 1.9
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PRIOR APPLICATION NUMBER: US '60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION UNBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                                                                                     Sequence 1861, Application US/09938842A Patent No. US20020160378A1
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Conservative
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SEQ ID NO 1861
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APPLICANT: Harper, Jeff
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Zhu, Tong
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GRAGIGGGIACACGCAGCIGIGCGACTACIGGAGCGIGGGCGICAICCIYIAYGAGAIGC 3947
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                                                                                                                                                                                                      · 3108 AGAATCAGCTGGAGAAGGAGATGCACAAAGTGGGACTGCCCGATCAGACCCCAAATCGAGA 3167
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                                                                                                                                                                                                                                                            3168 TGAGGAAAATGCTGAACCAAAAGGAGAGCAACTACATTCGATTGAAGCGCGCCAAGATGG
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                                                                                                                                                                             Indels
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                                                                                                                                                   Score 188.6; DB 10;
Pred. No. 7.4e-32;
2; Mismatches 356;
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PALENTIN VERSION 3.0
SEQ ID NO 89
LENGTH: 1818
                                                                                                                                                       3.3%;
                                                                                                                                                                       Similarity 54.99
                                                                                                                  ORGANISM: Homo sapiens
US-09-771-161A-89
                                                                                                                                                                                        Matches 469;
                                                                                                       TYPE: DNA
                                                                                                                                                             Query Match
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ACAGCTTCCAGGACAAGGATAATCTGTACTTTGTGATGGACTACATACCÀGGTGGTGATC 3497 

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240 IGTATGCAACAAAACTCTTCGAAAGAAAGATGTTCTTCTTCGAAATGAAGTCGCTCATG 3378 TGAAGGCCGAGAGATATCCTCGCGGAAGCCGACAATAACTGGGTGGTGAAGTTGTACT

3318 TGTATGCGATGAAAACCCTGCGGAAAGCGGACGTTCTCAAGCGGAATCAGGTGGCACACG

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3498 IGAIGICGCICCICAICAAACIGGGCAITII 3528

ACTACATTCGATTGAAGCGCGCCAAGATGGACAAGAGCATGTTCGTCAAACTGAAGCCCA 3257

TGGGACTGCCCGATCAGACCAAATCCAGAAAATGCTGAACCAAAAGGAGAGCA

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3258 TIGGAGIGGGIGCAITIGGCGAGGIAACGCIGGIGAGCAAAAICGAIACCICGAACCAIT 

3078 TCAAGTCGTATCGCCAGCGCACGTATCGCAAGAATCAGCTGGAGAAGGAGGTGCAAAAG 3137

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APPLICANT: Ford, Dona M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Lewis, Marcia E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/879,536
CURRENT FILING DATE: 2001-09-21
PRIOR FILING DATE: 1998-06-10
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Pred. No. 8.4e-27;
0; Mismatches 161;
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1) ... (678); OTHER INFORMATION: n = A,T,C OT G
                                                                                           Sequence 66, Application US/09879536
Patent No. US20020144298Al
                                                                                                                                                                                                             Burgess, Christopher C.
Bushnell, Steven E.
Carroll III, Eddle
Catino, Theodore J.
                                                                                                                                                        APPLICANT: Endege, Wilson O. APPLICANT: Steinmann, Kathleen APPLICANT: Astle, Jon H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.9%;
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Best Local Similarity 63.2
Matches 285; Conservative
1541 TCATCGGTAAGTTGC 1555
                                                                                                                                                                                                                                                                                            Derti, Adnan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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APPLICANT: Warg, Xun
APPLICANT: Warg, Xun
APPLICANT: Warg, Xun
APPLICANT: Warg, Xun
TITLE OF INVENTION: STRESS-RECULATED GENES OF PLANTS, TRANSÇENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF GE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-06-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 144.6; DB 9;
Pred. No. 3.1e-22;
0; Mismatches 174;
                                                                                                                                                                            Sequence 633; Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Arabidopsis thaliana US-09-938-842A-633
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Best Local Similarity 59.7%;
Matches 262; Conservative
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4033 GCCGCAGG 4040
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2001-06-14

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Query Match
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                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                           LENGIH:
                                                                                      APPLICANT: Wang, Xun
APPLICANT: DALY, TONG
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   603 GCAACTTAAATACTCTTTTCAGACCAAATACAGATTGTATCTTGTTCTTGACTTTATAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           663 CGGAGGTCATCTTCTTCCAGCTCTATCACCAAGGGCTTTTCAGGGAGGACTTGGCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          543 TGCTGAATACATGAAAGCCGAGCGCGATATTCTAACCAAAATCGATCATCCTTTCATTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1416;
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PPLICANT: Gene Logic, Inc.
ITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
ILE REFERENCE: 44921-5028-WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 138.6; DB 9;
Pred. No. 6.4e-21;
0; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/880,107
                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
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Patent No. US20020142981A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3667 CTTTGGCCTGTGCACGGGATT 3687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA ;
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.4%;
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Scherf, Uwe
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Matches 259; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 5379
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Patent No. US20020160378A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-880-107-2146
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 2503
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3239 TTCGTCAAACTGAAGCCCATTGGAGTGGGTGCATTTGGCGAGGTAACGCTGGTGAGCAAA 3298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3536 GAACTGGCCAGATTCTACATCGCCGAGGTCACCTGCGCCGTGGACAGCGTTCACAAAATG 3595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          290 GTCACCCGGCCTGACAGTGGGCACCTGTATGCTATGAAGGTGCTGAAGAAGGCAACGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        470 GACTICCIGCGIGGIGGGACCICTICACCCGGCICTCAAAAGAGGIGAIGTICACGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L07597
US-09-880-107-2146
                                                                                                                                                                                                                                                                                                                                                                                     Length 3061
                                                                                                                                                                                                                                                                                                                                                                                  DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                     Score 134.6; DB 1
Pred. No. 7.3e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/971,845 CURRENT FILING DATE: 2001-10-04 PRIOR APPLICATION NUMBER: PCT/US01/21479
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SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: DYSTROPHIA MYOTONICA
TITLE OF INVENTION: (DM-PK) AND ITS USES
PRIOR APPLICATION NUMBER: US 60/211,379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3656 AAGCTCACCGACTTTGGCCTGTGCA 3680
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PRIOR APPLICATION NUMBER: 60/238,558
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Patent No. US20020132247A1
                 FILING DATE: 2000-06-14
APPLICATION NUMBER: US 6
FILING DATE: 2000-10-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2146
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APPLICANT: DELANEY, ALLEN
                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
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Matches 258; Conserv
                   PRIOR FILING DATE:
PRIOR APPLICATION N
PRIOR FILING DATE:
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US-09-971-845-1
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TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION UNBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 133; DB 9; Length 36
Pred. No. 5.4e-20;
0; Mismatches 105; Indels
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SOFTWARE: FastSEQ for Windows Version 3.0
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  PRIOR APPLICATION NUMBER: 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR APPLICATION NUMBER: 60/23,378
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-07
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PRIOR FILING DATE: 2000-10-02
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APPLICANT: Horne, Darci T.
                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: unsure
CATION: (19)
CTHER INFORMATION: n=A,T,C or G
US-09-796-692-7789
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Best Local Similarity 65.13
Matches 196; Conservative
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SOFTWARE: Patentin Ver. 2.
                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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ORGANISM: HOMO S
FEATURE:
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                                                                                                                                                                                                                                      SEQ ID NO 7789
LENGTH: 362
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PPLICANT: Mannion, Jane
ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIACNOSIS AND THERAPY
TLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
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                                                                                                                                                              3190 GGAGAGCAACTACATTCGATTGAAGCGCCCCAAGATGGACAAGAGCATGTTCGTCAAACT 3249
                                                                                                                                                                                                                                                      3250 GAAGCCCATTGGAGTGGGTGCATTTGGCGAGGTAACGCTGGTGAGCAAAATCGATACCTC 3309
                                                                                                                                                                                                                                                                                                                                                                                          1055 GGCCCAGGTGTATGCCATGAAGATCATGAACAAGTGGGACATGCTGAAGAGGGGCGAGGT 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                     3370 GGCACACGTGAAGGCCGAGAGGGATATCCTCGCGGAAGCCGACAATAACTGGGTGGTGAA 3429
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                                                                                                                                                                                                                                                                                   1115 GTCGTGCTTCCGTGAGGAGGGACGTGTTGGTGAATGGGGACCGGCGGTGGATCACGCA 1174
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                                                                                                                                                                                                         938 GGAGCCCATCGTGGTGAGGCTTAAGGAGGTCCGACTGCAGAGGGACGACTTCGAGATTCT 997
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                                                                                                                     Indels
                                                                     Score 134.6; DB 10;
Pred. No. 7.7e-20;
0; Mismatches 204;
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"URRENT PILING DATE: 2001-03-03

RIOR ADDITON: 001200

RIOR ADDITON: 001200
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FILING DATE: 2000-05-22
                                                                     2.48;
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                                                                                           Best Local Similarity 57.4 Matches 283; Conservative
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US-09-971-845-1
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                                                                       Query Match
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3238 GTTCGTCAAACTGAAGCCCATTGGAGTGGGTGCATTTGGCGAGGTAACGCTGGTGAGCAA 3297 3298 AATCGATACCTCGAACCATTTGTATGCGATGAAAACCCTGCGGAAAGCGGACGTTCTCAA 3357 3358 GCGGAATCAGGTGGCACACGTGAAGGCCGAGGGGATATCCTCGCGGAAGCCGACAATAA 3417, 3418 CTGGGTGGTGAGTTGTACTACAGCTTCCAGGACAAGGATAATCTGTACTTTGTGATGGA 3477 3478 CTACATACCAGGIGGIGGICTCGAIGICGCTCATCAAACIGGGCAITIICGAGGAGGA 3537 3538 ACTGGCCAGATTCTACATCGCCGAGGTCACCTGCGCCGTGGACAGCGTTCACAAAATGGG 3597 241 CCAGGAGACCGGCGGCGCA---CTACGCCATGAGGACACACAGAGGGGGGGGAA 297 Gaps 358 GTTCCTCGTCAACTCCTCTTTAAGGACAACTCCTACTGTACCTGGTGATGGA 417 ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M34182 US-09-880-107-2340 Score 127; DB 10; Length 1635; Pred. No. 2.5e-18; 0; Mismatches 190; Indels 3 3658 GCTCACCGACTTTGGCCTGTGCACGGG 3684 Query Match, 2.2%; Best Local Similarity, 56.8%; Matches 254; Conservative õ g ò qq

Search completed: January 16, 2003, 22:07:03 Job time : 303.731 secs

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AL211543 Tetraodon
BM174548 Tm_ad_30G
AL594372 vo15f09.y
AA592233 vo15f09.r
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AY104378 Zea mays
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AL191564 Tetraodon
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BI290748 UI-R-DK0-
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AW563655 LG1_245_H
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN12B11 of DrosBAC library from Drosophila melanogaster (fruit
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Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
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/clone="BACN12B11"
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B1637464 Sprime SD Drosophila melanogaster Schneider L2 cell culture por2 Drosophila melanogaster Schneider L2 cell culture por2 Drosophila melanogaster cDNA clone SD19495 5 similar to wts: FBan0012072 GO: [protein phosphorylation (GO:0006468); protein serine/threonine kinase (GO:0004674); eye morphogenesis (GO:0007456); protein serine/threonine kinase (GO:0004674); protein kinase (GO:0004674); protein kinase (GO:0004674); protein kinase
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htt genomic AE003775: arm:3R [26377421,26613529]
estimated-cyto:100A3-100B2: 05/19/2001
Plate: SD.194 row: H column: 11
                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 662)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang
Lewis,S. and Rubin,G.M.
BIGP/HHMI Drosophila EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="vector: por2; Site_1: EcoRI; Site_2: Xhol; if ractionated cDRAs were directly ligated into por2 lasmid cDNA library." 1200 c. 190 g. 118 t.
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/db_xref="taxon:7227"
/clone="SD19495"
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ilarity 99.2%; Pred. No. 5.2e-103;
Conservative 1; Mismatches 0; 1
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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Location/Qualifiers
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657; Conserv
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241 GA			1311 AG 11 361 AG	1371 TA    			1491 AG	541 AG	551 AC       601 AC	611 GC	661 GC	,	າ ຜ	N			_		1			•			onrce					
Dp 5	1	-	QY 1.3 Db · 3	Qy 13			0y 14	Db 5	Qy 15 Db 6	Qy 16	Db 6		RESULT 3 B0898648	LOCUS	ACCESSION VERSION	KEYWORDS SOURCE	ORGANISM	AUTHORS TITLE	COMMENT					FEATURES	S					

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737 bp mRNA linear EST 14-MAR-2D02
UI-MEHDp-buu-b-12-0-UI.rl NIH_BMAP_EHOp Mus musculus cDNA clone
INAGE:5686955 5', mRNA sequence.
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5'-GACTAGTTCTAGATCGCGAGCGCCCCT(15)-3'. Size selected's lab for average insert length 1.7 Kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies. Technologies and the property of the same series of Medicine and 18 available through Life 18 229 c. 261 g 174 t.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
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                                                                                                                                                                                               Score 340.8; DB 14; Length 930;
Pred. No. 6.4e-50;
0; Mismatches 202; Indels 4;
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Best Local Sim
Matches 486;
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9   GGTGAGCAAAATCGATACCTCC   1   1   1   1   1   1   1   1   1   1		Ephydroide, Ewis, S  I (bases) Harvey, S  Lewis, S  Ewis, S  BDGP/HMI Unpublishe Contact: 8 BDGP Lawrence B DGP Ex: 510 4 Email: htt Based upon Sequence h Plate: 280 High quali I
OY .3289 Db 370 OY 3349 OY 3409 Db 487 OY 3469	OY 3529  Db 607  OY 3889  Db 667  OY 3649  Db 727  RESULT 5 AL517339 LOCUS  DEFINITION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT SOUIC SOUIC BASE COUNT
Name and the continuents are considered by the considering the continuents of Health, Mammalian Gene Collection (MGC) (Attonal Institutes of Health, Mammalian Gene Collection (MGC) (Attonal Institutes of Health, Mammalian Gene Collection (MGC) (Attonal Institutes of Health, Mammalian Gene Collection (MGC) (Attained (1999) (Contact: Robert Strausberg, Ph.D. (Contact: Robert Strausberg, Ph.D. (Contact: Robert Strausler) (Consecretion of Instance Contact: Dames Lib. (Consecretion of Instance Contact: Consecretion of Invariaty of Iowa Contact: Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa Contact: Distribution: MGC clone distribution information can be cond through the I.M. A.G.E. Consortium/LLNL at: This clone was contributed by the Brain Molecular Anatomy Project BMAPP)	r: pYx.5.  I. 737  /organism="Mus musculus"  /organism="C5BE16"  /organism="C5BE16"  /db xref="taxon:1090"  /clone="IMAGE:5686955"  /clone="Inage="map."  /dev_stage="embryo 18.5 dpc"  /lab_host="bill08"  /lab_host="bill08"  /lab_host="bill08"  /lab_host="bill08"  /lab_host="bill08"  /lab_host="bill08"  /lab_host="bill08"  /clone="Inage" /lab_host="bill08"  /clone="Inage" /clone in yetcor: px.xac; Site_1: EcoR I; /lab_host="bill08"  /clone in yetcor: px.xac; Site_1: EcoR I; /lab_host="bill08"  /clone="cording to px.xac; Site_1: EcoR I; /clone in yetcor: px.xac; Site_1: EcoR I; /clone in yetcor: px.xac; Site_1: EcoR I; /clone="cording to px.xac; Site_1: EcoR I; /clone="cording to px.xac; Site_1: EcoR I; /clone="cording to px.xac; Site_1: EcoR I; /clone="cordina" /clone="cordina	98; Score 334.8; DB 14; 18; Pred: No. 7.6e-49; 0; Mismatches 213; I CAGCCTCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
Mainmali 1 (bas NIH MGC NIH MGC Nationa (orpubli Contubli	Seq prime	209 tch. al Simila 505; Co CodGTGGAGA CHILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES SOUICE	BASE COUNT OWELY MA Best Loc Matches QY 2929 Db 72 QY 3049 Db 131 QY 3109 CY 3169 Db 190 CY 3169 Db 250 CY 3169

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644 bp mRNA linear EST 19-APR-2001
Drosophila melanogaster head poT2 Drosophila
clone GH2803 5prime similar to U29608: wts
03942 SPTREMBL:Q24096, mRNA sequence.
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= "adult".

= "bh" - lpha".

gan: head; Vector: pOT2; Site_1: EcoRI; Site_2: ed fractionated cDNAs were directly ligated into asmid ONAs library."
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G.M.
La EST Project
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Mus musculus cDNA clone IMAGE:5135667 5',
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 689)
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/clone_libe_NCI_CGAP_Li9"
/lab_host-"bH10B (TI phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1:9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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                                                       1223 CAGAATTACACACCTCTGCGATACACGGCGACCAACGGACGCAACGATGCACTTACTCCT 1282
                                                                                                              GACTATCACCACGCCAAGCAGCCGATGGAGCCGCCACCCTCCGCCTCTCCTGCTCCGGGAC 1342
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.
Plate: LLAM11333 row: h column: 04
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                               Gaps
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 Length 644;
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              Pred. No. 2.5e-46;
                            1; Mismatches
5.6%; Score 320.6; 99.7%; Pred. No. 2.5
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304; DB 13; Length 689; No. 2e-43;

Score Pred. 1

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Query Match Best Local Similarity

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CNS0396F 962 bp DNA linear GSS 15-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 006F24 of library G from Tetraodon nigroviridis, genomic survey
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
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Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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  Gaps
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Cost-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fis
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.
Saurlin, W. and Weissenbach, J.
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Mismatches
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AUTHORS
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Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

Chordata; Primates;

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/note="Organ: Pancreas; Vector: pSPORTI; Site_1: Not 1; Site_2: Sal 1: Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). CDNA made by Oligo-dry Priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on Solid support and plasmid DNA from library was prepared. The library DNA was normalized by Research 6:791-806; O.5 micrograms single-stranded library Research 6:791-806; O.5 micrograms single-stranded library representing library inserts and hybridized to an Ecot of Solids-stranded (unhybridized to an Ecot of Normal Solids-stranded (unhybridized by Plasmid Solids-stranded (unhybridized by Plasmids were isolated to the solid of Normal Solids of Solids Solids of Solids Solids of Solids Solids of Solids Solids of Solids Solids of Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids Solids
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Upublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enail: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Welton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IMAGE
consortium, for clone orders contact: info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                               Endocrine Pancreas Consorthum
Barvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
                                                                                                                                                                                                                                                                                                     Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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Location/Qualifiers
                                                        Mammalia; Eutheria;
1 (bases 1 to 590)
                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 617-495-1812
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       Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                   nigroviridis
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/note="Genoscope sequence ID : C0BG006DC12LP1-end : T7"
303 c 282 g 176 t l others
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                                                                                                                                                                    This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                                                                                                                                                       /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="006F24"
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Pred. No. 7.1
                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                           Direct Submission
Submitted (12-APR-2000)
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                                                                             (bases 1 to 962)
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/clone\_lib="Melton Normalized Human Islet 4 N4-HIS 1"

/organism="Homo sapiens" /db\_xref="taxon:9606"

/clone="IMAGE:5672052"

/sex="Both"

/tissue\_type="Islets of Langerhans"

/dev\_stage="Adult" /lab\_host="DH108"

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3063 ACATAGAGAACGTGATCAAGTCGTATCGCCAGCGCACGTATCGCAAGAATCAGCTGGAGA 3122
                                                                                                                                                                                                                                                               ACCAAAAGGAGAGCAACTACGATTGAAGCGCGCCAAGATGGACAAGAGCATGTTCG 3242
                                                                                                                                                                                                                                                                                                                     3243 TCAAACTGAAGCCCATTGGAGTGGGTGCATTTGGCGAGGTAACGCTGGTGAGCAAAATCG 3302
                                                                                                                                                                                                                                                                                                                                                                         3303 ATACCTCGAACCATTTGTATGCGATGAAAACCCTGCGGAAAGCGGACGTTCTCAAGCGGA 3362
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                                                                                                                                                                                                       3123 AGGACATGCACAAAGTGGGACTGCCCGATCAGACCCAAATCGAGATGAGGAAAATGCTGA
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                                                                                                    DB 13;
                                                                                                Score 291.2; DB 13;
Pred. No. 3.6e-41;
0; Mismatches 178;
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GI:16808642

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ACCESSION VERSION KEYWORDS Homo sapiens

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Homo sapiens
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Endocrine Pancreas Consortium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Höminidae, Homo.
1 (bases 1 to 579)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pSPORT1; Site_1: Not 1;
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                                                                                                                                                 3423 IGGIGAAGITGIACIACAGCTICCAGGACAAGGAIAAICIGIACITIGIGAAGGACIACA 3482
                                                                                                                                                                                                                                        TACCAGGTGGTGATCTGATGTCGCTGCTCATCAAACTGGGCATTTTCGAGGAGGAACTGG 3542
                                                                                                                                                                                                                                                                                                                           CCAGATTCTACATCGCCGAGGTCACCTGCGCCGTGGACAGCGTTCACAAAATGGGCTTCA 3602
                                                                                                                                                                          241 A---CACTCACGCCTGTACGCCATGAAGACCCTAAGGAAAAGGATGTCCTGAACGGGA. 297
                                                                                         418 TCCCTGGTGGGGACATGATGAGCCTGCTGATCCGGATGGAGGTCTTCCCTGAGCACCTGG 477
                                                                                                                                                                                                                                                                                                                                                                   478 CCCGGTTCTACATCGCAGAGCTGACTTTGGCCATTGAGAGTGTCCACAAGATGGGCTTCA 537
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                                                                3363 ATCAGGIGGCACACGIGAAGGCCGAGAGGGAIAICCICGCGGAAGCCGACAAIAACIGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (brown)efas.harvard.edu) This sequence now available from toonsortium, for clone orders contact: info@image.llnl.gov High quality sequence stop: 432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endocrine Pańcreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave,
                                                                                                                                                                                                                                                                                                                                                                                                            'tissue_type="Islets of Langerhans"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'clone="IMAGE:5671888"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BI964175.1 GI:16338580
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ORGANISM

REFERENCE AUTHORS JOURNAL

TITLE COMMENT FEATURES

ACCESSION VERSION KEYWORDS SOURCE

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library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of SO. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bp mRNA linear EST 05-MAR-2002
Homo sapiens cDNA clone IMAGE:5560599
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Mammalia; Eutherita; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 957)
NIH-MGC http://mgc.ncl.nih.gov/.
                          Library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3123 AGGAGATGCACAAAGTGGGACTGCCCGATCAGACCCAAATCGAGGAAAATGCTGA 3182
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  made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library we amplified once on solid support and plasmid DNA from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCAGGTGGCACACGTGAAGGCCGAGAGGGATATCCTCGCGGAAGCCGACAATAACTGGG
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oligo-dT priming. Size-selected
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                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                      .7e-40;
                                                                                                                                                                                                                                                                                                                                Score 284.4;
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AGENCOURT_6459219 NIH_MGC_88
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BM801311
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Query Match
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 AGGAAAAAGGATGTCCTGAACCGGAATCAGGTGGCCCACGTCAAGGCCGAGGGGACATC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            480 CACAATTCCAAATATTACC---AGAAAGGGAGCCATGTCAGAACAGGACAGCATGGAGCCC 536
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                           /clone_lib="NIH_MGC_88"
/clone_lib="NIH_MGC_88"
/tissue_lype="duodenal adenocarcinoma, cell line"
/tissue_rype="duodenal adenocarcinoma, cell line"
/tishost="DH10B (hange-resistant)"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site_1: Not1; Site_2: Sall; Cloned unidirectionally;
                                                                                        CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12287 row, a column: 16
High quality sequence stop: 485.
Location/Qualifiers
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6
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Pred. No. 2e-39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 145;
                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"/db_xref="taxon:9606"
                                      Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                  Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.9%;
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lactis var. lactis, Kluyeromyces marxianus var. marxianus, prichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See theywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This GSS is part of a remove sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(<4. .>1001)
/note="similar to Saccharomyces cerevisiae ORF YNL161w [
CBK1 ; strong similarity to U.maydis Ukclp protein kinase
      GSS 08-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
CNSO77GT 1006 bp DNA linear GSS 08-JUL-200 T7 end of clone BBOAA011G01 of library BBOAA from strain CBS 4732 of Pichia angusta, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 1006)
Blandin,G., Llorente,B., Malpertuy,A., Wincker,P., Artiguenave,F.,
and Dujon,B.
                                                                                                                                                                             Pichia angusta.
Pichia angusta
Pichia angusta
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCGTCAAACTGAAGCCCCATTGGAGTGGGTGCATTTGGCGAGGTAACGCTGGTGAGCAAA 3298
                                                                                                                                                                                                                                                                                                           ( Pases 1 to 1006)
Souciet, J. L., Agle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S. Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           950 TICCACACACACATCATCGCAAGGSGCCYTITGGCGAGGTCCGACTCGTCCAAAAA 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomic exploration of the hemiascomycetous yeasts: 13. Pichia
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Pred. No. 4.9e-38;
6; Mismatches 346;
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.269 c 272 g 249 t
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/clone="BB0AA011G01"
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                                                                                                      AL432675
AL432675.1 GI:12216089
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Matches 542; Conservative
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Brachycera;
                                                                                                                                                                                                                                                                                                                                                        Score 262; DB 13;
Pred. No. 5.9e-36;
); Mismatches 0;
       Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 280)
Harvey, D., Brokstein, P., Hong, L., Evans Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausherg, Ph.D.
Tissue Procurement: DCTb/DTP/Gazdar
                                                                                                                                                                                                                                                                      /lab_host="DH5-alpha"
                                                                                                                                                                                                                                                                                                                                                        4.6%;
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                                                                                  Contact: Stapleton,
                                                                                                                                                                                                                                                                                                                                                                                  Matches 276; Conservative
                                                                     Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
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AUTHORS
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                     REFERENCE
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                                  AUTHORS
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L2 cell culture
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTACGGACTTGATAAGGAGGCTCTGTGCGTCGGCTGACAAGCGGGCTGGGCAAGAGCGTG 4117
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                    ပ္ပ
                                                                                                                                                                                                                                                                                                                                                                      354 AAATCCAGACGCTCATGCCGTACCTACCGTCGGAACTCCCGGCTACATTGCTCCAGAG
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                                                                                                        TGGGTGGTGAAGTTGTACTACAGCTTCCAGGACAAGGATAATCTGTACTTTGTGATGGAC
                                                                                                                                                                                                        CTGGCCAGATTCTACATCGCCGAGGTCACCTGCGCCCGTGGACAGCGTTCACAAAATGGGC
                                                                                                                                                                                                                                                       3659 CTCACCGACȚTTGGCCTGTGCACGGGATTCCGATGGACGCACAACTCGAAGTACT----
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Drosophila melanogaster
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601483053F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3885780 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="SD Drosophila melanogaster Schneider L2 cell
culture por2"
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Su, C., Tsang, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGCGGAGCATTTCTGTGATATGAGTGCTAAATGCCACAGGGCGAAGCAGCAGCATCATG 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             930 AAAAATAATAATAATCGTAGAGAGGCAGAGCCAAAATCAAATTCCCGGCCGCCGATGTGCC 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 CATCCAGCGGCGGAAAAAAGGGGGCGGTCGCCCCAATGATAAATACACGGGGGAAGCCCTC 240
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 863)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                             Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA One Cyclotron Rd, Berkeley, CA 94720, USA Exa: 510 466 6798

Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu plate: SD.268 row: E column: 5

High quality sequence stop: 277.

Location/Qualifiers
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fractionated cDMAs were directly ligated into pOT2:
Plasmid cDNA library."
1 60 68 9 59 t
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                                                                                                                                                                                                                                                                                                                                                                                     /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="SD26853"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGAGCATCAAGCAGGACCTAACCCGATTTGAAGTACAAA 1205
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/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggcgctcggcc); Site_2: Sfil (ggcattatggcc); 5' and
sequence: S'-GacGGCGATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCGGAGGGGCGCATG-dT(30)BN-3' (where B = A,
c' or G and N = A, c' G, or T). Average insert size 1:9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR: This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NHLMC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3533 GAGGAACIGGCCAGAITCTACAICGCCGAGGICACCIGCGCCGIGGACAGCGITCACAAA 3592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3653 ATAAAGCTCACCGACTTTGGCCTGTGCACGGGATTCCGATGGACGCACAACTCGAAGTAC 3712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACCANAGAGTCCTGGCCCACTCGCTGGTGGCCACCCCGGAACTACATAGCTCCCGAGGTG 3880
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                        http://mgc.nci.nih.gov/.
Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 ATTAAACTCACAGATTTCGGCCTCTGCACTGGGTTCAGGTGGACTCACAATT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 ATGGGCTTCATCCACCGAGACATCAAGCCTGATAACATTTTGATAGATCTGGATGGTCAC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) NA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution: MGC clone distribution information or found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov p. Plate: LLCM1511 row: p column: 04 High quality sequence stop: 570.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3713 TACCAGGA-----GAACGGCAATCACTCGCGCCAGGACTCGATGGAGCCCTGGGAGGA-
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                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="NIH_MGC_77"
/lab_host="DH10B (T1 phage-resistant)"
                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 255.2; DB 12;
Pred. No. 7.1e-35;
3; Mismatches 236;
                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                       Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:4691955"
                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                     Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.58;
                                                                 Unpublished (1999)
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                                                                                                                                                                                                                                                                                                       /tissue_type="large cell carcinoma, undifferentiated"
/lab_host="DH10B (phage-resistant)"
/note="Norgan: lung: Vector: pCMV-SPORT6; Site_1: Not!;
Site_2: SAll; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.1 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG538495 73-407 APR-2001 10.02567216F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4691955 5',
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CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution and clone distribution on the Consortium found through the I.M.A.G.E. Consortium found.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3318 TGTATGCGATGAAAACCCTGCGGAAGCGGACGTTCTCAAGCGGAATCAGGTGGCACACG 3377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3438 ACAGCTICCAGGACAAGGAIAAICIGIACTITGIGAIGGACTACAIACCAGGIGGIGAIC 3497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 TGTACGCCATGAAGACCCTAAGGAAAAAGGATGTCCTGAACCGGAATCAGGTGGCCCACG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 rGATGAGCCTGCTGATCGGGATGGAGGTCTTCCCTGAGCACCTGGCCCGGTTCTACATCG 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3618 AGCCTGACAACATACTCATCGATAGGGACGGACACATAAAGCTCACCGACTTTGGCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; B
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
I (bases I to 736)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10;
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Pred. No. 4.5e-35;
0; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                      166 t
                                                                                                             http://image.linl.gov
Plate: LLAM9661 row: i column: 13
High quality sequence stop: 706.
                                                                                                                                                                                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                 /clone_lib="NIH_MGC_69"
                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone="IMAGE:3885780"
                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                    271 g
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Best Local Similarity 75.1'
Matches 334; Conservative
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BG538495
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BASE COUNT ORIGIN

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Gaps

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Indels

Length 736;

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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE

DEFINITION

ACCESSION

RESULT 14 BG538495

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Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.n column: 16
                                                                                                                                                                                                                                                                                                          BI525737 824 bp mRNA linear EST 29-AUG-2001 602926563F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5059023 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 824)
4060 TACGGACTIGATAAGGAGGCTCTGTGCGTCGGCTGACAAGCGGCTGGGCAAGAGCGTGGA 4119
                                                            1120 CGAGGTCAAGAGCCA--CGACTTCTTCAAGGGCATCGACTT----TGCGGACATGCGGAA 4173
                                                                                              662
                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                    543 CAGGGACCTCATCACCAAGCTGTGCTGCTCCAGAGACCAGCTGGGCGGAATGGGGCGA
                                                                                           603 TGACCTGAAGGGCCAACCCCATTCTTCAGGGCCCAATGACTTCTCCAGTGACCATCGGAA
                                                                                                                            GCAGAAAGCGCCCTACATACCGGAAATCAAGCACCCRACGGACACATCCAACTTTGATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="pooled_lung tumors"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plate: LLAM11159 row: n column: 16
High quality sequence start: 10
High quality sequence stop: 745.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
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/clone="IMAGE:5059023"
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                                                                                                                                                                                             CGTGGATCCGGAGA 4247
                                                                                                                                                                                                                      722 CGTAGATGAAGAA 735
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                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                         house mouse
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BI525737/c
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DEFINITION
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AUTHORS
TITLE
JOURNAL
COMMENT
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                                                                                                                                                             663
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KEYWORDS
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Gaps

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Indels

Length 824;

DB 13;

Score 255.2; DB 13; Pred. No. 6.9e-35; 2; Mismatches 190;

4.5%; nilarity 68.6%; Conservative 2

Query Match Best Local Similarity Matches 473; Conserve

ORIGIN

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3854 ACCCCGAACTACATAGCTCCCGAGGTGCTGGAGAAGRAGTGGGGTACACGCAGCTGTGCGAC 3913
                                                                                                                                                                                                                                              GACAAGGATAATCTGTACTTTGTGATGGACTACATACCAGGTGGTGATCTGATGTCGCTG 3508
                                                                                                                                                                                                                                                                                                                                                                    CTCATCAAACTGGGCATTTTCGAGGAGGAACTGGCCAGATTCTACATCGCCGAGG-TCAC 3567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3568 CTGCGCCGTGGACAGCGTTCACAAATGGGCTTCATTCACAGAGACATCAAGCCTGACAA 3627
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3334 CCTGCGGAAAGCGGACGTTCTCAAGCGGAATCAGGTGGCACA--CGTGAAGGCCGAGAGG
                                      281 GACCTGGAGGGGGGGGGGGGGAGAGGAGGGGGGGCTGGCAATTCTCTTGTCGG
                                                                                                                     GATATCCTCGCGGAAGCCGACAATAACTGGGTGGTG--AAGTTGTACTACAGCT-TCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 ACACCAAATTACATCGCTCCGGAGGTGCTTCTCCGCAAAGGGTACACGCAGCTCTGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGCTGGAGAGGCGACGGATGCGCGATCACCAAAGAGTCCTGGCCCACTCGCTGGTGGGC
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Job time: 4988.5 secs
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